

STIC-Biotech/ChemLib

143098

ms

From: Fredman, Jeffrey  
Sent: Tuesday, January 25, 2005 6:06 AM  
To: STIC-Biotech/ChemLib  
Cc: Schultz, James  
Subject: FW: RUSH sequence search 09/828,870

PLEASE RUSH.

I Approve.

Jeff Fredman

-----Original Message-----

From: Schultz, James  
Sent: Monday, January 24, 2005 5:16 PM  
To: Fredman, Jeffrey  
Subject: RUSH sequence search 09/828,870

Hi Jeff,

If you approve the following rush request, could you please forward this to STIC-biotech? This case was a transfer for which I thought the sequence searches had been ordered. There are two sequences because they have been disclosed as useful together.

Thanks,  
Doug Schultz

STIC searchers,

Could you please run RUSH standard amino acid sequence searches against both SEQ ID NOS:36 and 39 (both 20 aa long) in the above entitled case?

Thanks,  
Doug Schultz

James Douglas Schultz, PhD  
AU 1635 (Biotechnology)  
Patent Examiner  
United States Patent and Trademark Office  
(Office) REM 2D18  
(Mail) REM 2C18  
(571) 272-0763

\*\*\*\*\*

STAFF USE ONLY

Searcher: Jan  
Searcher Phone: 2- 2504  
Date Searcher Picked up: 1/25/05  
Date Completed: 1/26/05  
Searcher Prep/Rev. Time: 10  
Online Time: 5:15

\*\*\*\*\*

Type of Search

NA Sequence: # \_\_\_\_\_  
AA Sequence: # ✓  
Structure: # \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: ✓  
WWW/Internet: \_\_\_\_\_  
Other(Specify): \_\_\_\_\_

**This Page Blank (uspio)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 26, 2005, 00:05:26 ; Search time 169 Seconds  
(without alignments)  
42.453 Million cell updates/sec

Title: US-09-828-870-36

Perfect score: 102  
Sequence: 1 TMGVGRQLAIGDINRRY 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04.\*  
1: geneseqp1980s.\*  
2: geneseqp1990s.\*  
3: geneseqp2000s.\*  
4: geneseqp2001s.\*  
5: geneseqp2002s.\*  
6: geneseqp2003as.\*  
7: geneseqp2003bs.\*  
8: geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	102	100.0	20	5 AAU77891	Aau77891 Bak GD bi
2	102	100.0	20	8 ADK14723	Adk14723 Bcl1-2 rel
3	102	100.0	26	3 AAY96322	Aay96322 Mammalian
4	102	100.0	26	4 AAB70372	Aab70372 BAK BH3 C
5	102	100.0	27	3 AAB37004	Aab37004 Bcl2 poly
6	102	100.0	28	2 AAU06294	AAU06294 GD domain
7	102	100.0	28	5 AAU77877	Aau77877 Bak GD do
8	102	100.0	28	8 ADK14689	Adk14689 Bcl1-2 rel
9	102	100.0	28	5 ADK14705	Adk14705 Bcl1-2 rel
10	102	100.0	36	5 AAU77889	Aau77889 Bak GD do
11	102	100.0	36	8 ADK14701	Adk14701 Bak GD do
12	102	100.0	152	2 AAR77879	Aar77879 Human Cdn
13	102	100.0	211	2 AAR77876	Aar77876 Human Cdn
14	102	100.0	211	2 AAR77877	Aar77877 Human Cdn
15	102	100.0	211	2 AAR81451	Aar81451 Bcl-Y apo
16	102	100.0	211	2 AAU03668	AAU03668 Bak prote
17	102	100.0	211	2 AAU03669	AAU03669 Bak-2 pro
18	102	100.0	211	2 AAW79534	AAW79534 Bak poly
19	102	100.0	211	2 AAY05433	Aay05433 Human BAK
20	102	100.0	211	5 ABB82374	ABB82374 Human BAK
21	102	100.0	211	6 AAE37655	AAE37655 Bcl2 rela
22	102	100.0	211	6 ABR47397	ABR47397 Breast ca
23	102	100.0	211	7 ADD93300	ADD93300 Human pro
24	102	100.0	211	7 ADP60830	ADP60830 Human Bak
25	102	100.0	211	8 ADL69726	ADL69726 Human Bcl

26	102	100.0	211	8 ADP04114	Adp04114 Human col
27	97	95.1	19	5 AAU77890	Aau77890 Bak GD bi
28	97	95.1	19	8 ADK14722	Adk14722 Bcl1-2 rel
29	97	95.1	117	2 AAW79535	AAW79535 Truncated
30	97	95.1	141	2 AAR77880	Aar77880 Human Cdn
31	92	90.2	27	3 AAB37005	Aab37005 Bcl2 poly
32	92	90.2	208	2 AAY05432	Aay05432 Mouse BAK
33	90	88.2	28	6 ABJ18893	Abj18893 Human Bcl
34	86	84.3	31	2 AAW06295	AAW06295 GD domain
35	86	84.3	31	5 AAU77878	Aau77878 Bak GD do
36	86	84.3	31	8 ADK14703	Adk14703 Bcl1-2 rel
37	86	84.3	31	8 ADK14690	Adk14690 Bcl1-2 rel
38	85	83.3	17	6 ABJ18903	Abj18903 Human Bcl
39	85	83.3	18	6 ABJ18823	Abj18823 Human Bcl
40	85	83.3	18	6 ABJ18862	Abj18862 Human Bcl
41	80	78.4	16	2 AAY05423	Aay05423 Human BAK
42	80	78.4	16	3 AAB37030	Aab37030 Bcl2 poly
43	80	78.4	16	4 AAB71977	Aab71977 Bak BH3 P
44	80	78.4	16	5 ABG78501	ABG78501 Mutant Bc
45	80	78.4	16	5 AAM52299	Aam52299 Miniature

ALIGNMENTS

RESULT 1  
AAU77891  
ID AAU77891 standard; peptide; 20 AA.  
XX AC AAU77891;  
XX DT 05-JUN-2002 (first entry)  
XX DE Bak GD binding domain derived peptide #2.  
XX KW GD domain; apoptosis; interaction with Bcl-XL; cell killing function;  
XX KW bak; cell death regulatory molecule; autoimmune disease; cancer; mutant;  
XX KW mteuin.  
XX OS Unidentified.  
XX OS Synthetic.  
XX PN US6221615-B1.  
XX PD 24-APR-2001.  
XX PF 25-JAN-1999; 99US-00236385.  
XX PR 12-MAY-1995; 95US-00440391.  
XX PR 08-AUG-1997; 97US-00908597.  
XX PA (APOP-) APOPTOSIS TECHNOLOGY INC.  
XX PI Chittenden TD, Lutz RJ;  
XX DR WPI; 2002-234950/29.  
XX PT Identifying agents (e.g. modulators of apoptosis) capable of modulating  
GD domain mediated heterodimerization or homodimerization comprises  
carrying out a heterodimerization or homodimerization assay.  
XX PS Example; Col 22; 37pp; English.  
XX CC The present invention relates to novel peptides, designated GD domains,  
which are capable of modulating apoptosis. The GD domains are essential  
for Bak's interaction with Bcl-XL, and to Bak's cell killing function.  
XX CC The GD domains mediate key protein/protein interactions with multiple  
cell death regulatory molecules. Also described are methods of  
identifying agonists or antagonists of GD domains. The methods are useful  
for identifying agents capable of modulating GD domain mediated  
heterodimerization or homodimerization. The methods are particularly  
useful in drug screening and design, e.g. for identifying modulators of  
treating autoimmune disease or cancer, or for identifying modulators of

CC apoptosis. The present sequence representing a Bak GD binding domain  
 CC derived peptide is used in the methods of the present invention

SQ Sequence 20 AA;

Query Match 100.0%; Score 102; DB 5; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-10;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TMGVGRLAIIGDDINRRY 20  
 |||||  
 Db 1 TMGVGRLAIIGDDINRRY 20

## RESULT 2

ADK14723  
 ID ADK14723 standard; peptide; 20 AA.

XX ADK14723;

AC 03-JUN-2004 (first entry)

DT BCL-2 related gene Bak residues 70-89 seqid 36.

DE anti-HIV; dermatological; immunosuppressive; antiinflammatory;  
 KW antirheumatic; antiarthritic; GD domain peptide; apoptosis;  
 KW protein domain; GD domain; bcl-2 related gene; Bak; cell death;  
 KW immunoreactive protein; degenerative disorder;  
 KW cell proliferation disorder; cell death disorder; autoimmune disease;  
 KW systemic lupus erythematosus; SLE; rheumatoid arthritis;  
 KW acquired immunodeficiency syndrome; AIDS.

XX Unidentified.

OS US2004054129-A1.

XX 18-MAR-2004.

XX 10-APR-2001; 2001US-00828870.

XX 12-MAY-1995; 95US-00440391.

PR 08-AUG-1997; 97US-00908597.

PR 25-JAN-1999; 99US-00236365.

XX (APOP-) APOPTOSIS TECHNOLOGY INC.

XX Chittenden TD, Lutz RJ;

XX WPI; 2004-247780/23.

XX Novel isolated and purified peptide comprising GD domain, useful for  
 PT treating degenerative disease e.g., rheumatoid arthritis.

XX Example; SEQ ID NO 36; 38pp; English.

XX The invention describes an isolated and purified peptide (I) comprising  
 CC unrecognised protein domain (GD domain) isolated from the bcl-2 related  
 CC gene Bak that can induce cell death. (I) is useful for identifying an  
 CC agent capable of modulating GD domain radiated heterodimerisation or  
 CC homodimerisation. (IV) is useful for screening a cDNA expression library  
 CC for clones comprising DNA inserts encoding immunoreactive proteins  
 CC (claimed). An anti-(I)-antibody, its mimetics, fragments, functional  
 CC equivalents and/or hybrids or its mutants, and a vector comprising a  
 CC polynucleotide encoding (I) are useful as agents for treating  
 CC degenerative disorders including disorders having inappropriate cell  
 CC proliferation or inappropriate cell death. The agents are also useful for  
 CC treating disorders in which a cell is present and/or persists in an  
 CC inappropriate location, and autoimmune disease such as systemic lupus  
 CC erythematosus (SLE) and rheumatoid arthritis. The degenerative disorder  
 CC include acquired immunodeficiency syndrome (AIDS). This is the amino acid  
 CC sequence of Bak residues 70-89, a variant of the GD domain uniquely  
 CC required for Bak's cell killing function.

SQ Sequence 20 AA;

Query Match 100.0%; Score 102; DB 8; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-10;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TMGVGRLAIIGDDINRRY 20  
 |||||  
 Db 1 TMGVGRLAIIGDDINRRY 20

## RESULT 3

AA96322  
 ID AA96322 standard; peptide; 26 AA.

XX AA96322;

XX 17-AUG-2000 (first entry)

DT Mammalian Bak Bcl-2 homology domain 3 domain.

DE Mammal; apoptosis; cell death; BBC3; apoptosis promotion; Bak;  
 KW apoptosis inhibition; malignant cell; autoimmune disease.

XX Mammalia.

OS WO200026228-A1.

XX 11-MAY-2000.

XX 28-OCT-1999; 99WO-US025285.

XX 02-NOV-1998; 98US-00184168.

XX (CLON-) CLONTECH LAB INC.

XX Zhu L, Yin X, Chittenden T;

XX WPI; 2000-365560/31.

XX Novel polynucleotide encoding a BBC3 protein which is useful for  
 PT modulating apoptosis, especially in the treatment of cancer and  
 PT autoimmune diseases.

XX Disclosure; Fig 4; 47pp; English.

XX The present sequence is the mammalian Bak Bcl-2 homology domain 3 (BH3)  
 CC domain, which was used in a sequence alignment with the same domain of a  
 CC putative version of the mammalian apoptosis regulator BBC3, which was  
 CC designated BBC3-ORF2. The BBC3 protein, nucleic acids and antibodies are  
 CC suitable for use in promoting cell death or for preventing apoptosis in  
 CC malignant cells and those causing autoimmune diseases

XX Sequence 26 AA;

Query Match 100.0%; Score 102; DB 3; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-10;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TMGVGRLAIIGDDINRRY 20  
 |||||  
 Db 1 TMGVGRLAIIGDDINRRY 20

## RESULT 4

AA96322  
 ID AA96322 standard; peptide; 26 AA.

XX AA96322;

XX 02-MAY-2001 (first entry)

XX BAK BH3 consensus peptide sequence SEQ ID NO:5.



KW Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;  
 KW immunostimulant; neuroprotective; nootropic; antiischemic; vulnary;  
 KW cytostatic; antiviral; antiarthritic; antiinflammatory; wound healing;  
 KW immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer;  
 KW immunodeficiency disease; neurodegenerative disease; viral infection;  
 KW ischaemic cell death; reperfusion cell death; arthritis; infertility;  
 KW lymphoproliferative condition; inflammation; autoimmune disease.  
 XX Unidentified.  
 OS WO200110888-A1.  
 PN PD 15-FEB-2001.  
 XX PF 30-MAY-2000; 2000WO-US011864.  
 XX PR 28-MAY-1999; 99US-0136783P.  
 XX PA (APOP-) APOPTOSIS TECHNOLOGY INC.  
 XX PI Zhou X;  
 XX WPI; 2001-138734/14.  
 DR New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide,  
 XX useful for screening for candidate compounds which induce or inhibit  
 PT apoptosis, comprises amino acid substitutions at Ser118, Ser155 or  
 PT Ser113.  
 XX Example 2; Fig 3a; 157pp; English.  
 XX The present invention describes an isolated or synthetic polypeptide (I)  
 CC comprising a less than full length amino acid sequence of a mutant Bcl-  
 CC XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its  
 CC fragment, which contains amino acid substitutions at Ser118 of a human  
 CC BAD, Ser155 of a murine BAD (longer murine BAD) or Ser113 of a murine BAD  
 CC (shorter murine BAD). (I) has immunostimulant, neuroprotective,  
 CC nootropic, antiischemic, vulnary, cytostatic, antiviral,  
 CC antiarthritic, antiinflammatory and immunosuppressive activities, and can  
 CC be used as an apoptosis inducer or inhibitor. BAD polypeptides and  
 CC polynucleotides can be used for screening candidate compounds and drugs  
 CC for activity that promote cell survival or apoptosis. Other uses include  
 CC inducing or inhibiting apoptosis in a cell. Candidate compounds  
 CC identified and (mutant) BAD polypeptides are useful in treating  
 CC immunodeficiency diseases, neurodegenerative diseases, ischaemic cell  
 CC death, reperfusion cell death, wound healing, cancer, viral infections,  
 CC lymphoproliferative conditions, arthritis, infertility, inflammation and  
 CC autoimmune diseases. The present sequence represents a Bcl-family member  
 CC BH3 domain consensus sequence which is used in an example from the  
 CC present invention  
 XX Sequence 26 AA;  
 SQ  
 Query Match 100.0%; Score 102; DB 4; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-10;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TMGQVGRQLAIGDDINRRY 20  
 DB 1 TMGQVGRQLAIGDDINRRY 20  
 RESULT 5  
 AAB37004  
 ID AAB37004 standard; peptide; 27 AA.  
 XX AAB37004;  
 XX 28-FEB-2001 (first entry)  
 DT Bcl2 polypeptide BH3 domain peptide #4.  
 DE  
 XX

KW Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective;  
 KW cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad;  
 KW apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;  
 KW colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;  
 KW melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS; stroke;  
 XX myocardial infarction.  
 OS Homo sapiens.  
 XX WO200059526-A1.  
 PN PD 12-OCT-2000.  
 XX PF 06-APR-2000; 2000WO-US009352.  
 XX PR 07-APR-1999; 99US-0128202P.  
 XX PA (UWJE-) UNIV JEFFERSON THOMAS.  
 XX Huang Z, Wang J, Zhang Z, Shan S, Lu Z;  
 PI WPI; 2000-679325/66.  
 DR New peptide conjugates for modulating apoptosis or for inhibiting B cell  
 PT lymphoma/leukemia 2 (Bcl-2) function, especially useful for treating  
 PT neurodegenerative disorders, stroke, or cancer.  
 XX Claim 18; Page 17; 74pp; English.  
 XX The invention relates to a peptide conjugate having the formula: (R-X)n-  
 CC peptide where n = 1-10; X = C=O, when the R-X group is attached to the N-  
 CC terminus of the peptide, or a side chain of the peptide where the  
 CC functional group of the side chain is NH2 or OH; or X = O or NH, when the  
 CC R-X group is attached to the C-terminus of the peptide, or a side chain  
 CC of the peptide, where the side chain functional group is COOH or CONH2;  
 CC and R = 2-18C alkyl or alkoxy, 2-14C alkylenyl containing one or two  
 CC double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally  
 CC monosubstituted with a 1-5C straight or branched chain alkyl group,  
 CC phenyl optionally monosubstituted with a 1-5C straight or branched chain  
 CC alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples  
 CC of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of  
 CC the BH3 domain of the cell death agonist Bad. The peptide conjugate is  
 CC useful for modulating apoptosis in the cells of a subject, or for  
 CC reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of  
 CC apoptosis in cancer cells. It is also useful for inhibiting Bcl-2  
 CC function. In particular, the peptide conjugate is useful for treating a  
 CC subject afflicted with a cancer characterized by cancer cells that  
 CC express Bcl-2. The cancer includes prostate, colorectal, gastric, non-  
 CC small lung, renal or thyroid cancers, neuroblastoma, melanoma, or acute  
 CC or chronic lymphocytic and non-lymphocytic leukemia. The peptide  
 CC conjugate is also useful for treating disorders characterized by  
 CC increased apoptosis, e.g. neurodegenerative disorders, acquired  
 CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction  
 XX Sequence 27 AA;  
 SQ  
 Query Match 100.0%; Score 102; DB 3; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-10;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TMGQVGRQLAIGDDINRRY 20  
 DB 4 TMGQVGRQLAIGDDINRRY 23  
 RESULT 6  
 AAW06294  
 ID AAW06294 standard; peptide; 28 AA.  
 XX AAW06294;  
 XX 29-JUL-1997 (first entry)  
 DT

XX DE GD domain region for Bak amino acid residues 67-94.  
 XX KW Apoptosis; follicular lymphoma; tumour; p53; antibody.  
 XX OS Synthetic.  
 XX PN WO9635951-A1.  
 XX PD 14-NOV-1996.  
 XX PF 06-MAY-1996; 96WO-US006122.  
 XX PR 12-MAY-1995; 95US-00440391.  
 XX PA (IMMU-) IMMUNOGEN INC.  
 XX PI Chittenden TD, Lutz RJ;  
 XX DR WPI; 1996-518805/51.  
 XX DR N-PSDB; AAT42428.  
 XX PT Peptide(s) comprising GD domains - have similar activities to wild type  
 XX PT Bak, and cause cellular apoptosis for treatment of viral infection.  
 XX PS Claim 2; Page 52; 69pp; English.  
 XX CC The term GD domain refers to a protein domain first identified in Bak and  
 CC shown to be essential for the interaction of Bak with Bcl-x(L) and for  
 CC Bak's cell killing function; and to peptides and/or molecules capable of  
 CC mimicking its structure and/or function. The present sequence represents  
 CC a GD domain corresponding to amino acid residues 67-94 of Bak. An  
 CC antibody raised against a GD domain may be used to screen a cDNA  
 CC expression library for clones comprising cDNA inserts encoding  
 CC immunoreactive proteins. Truncated GD domain peptides have been  
 CC shown to maintain the protein binding and cell killing function exhibited  
 CC by wild type Bak. These molecules may induce apoptosis in tumour cell.  
 CC These peptides act independently of p53 status. Bak or GD domain mimetics  
 CC that inhibit Bcl-2 may be selectively toxic to certain tumours, e.g.  
 CC follicular lymphoma, which depend on high levels of Bcl-2 for their  
 CC continued growth and survival. GD domain mimetics may also be used for  
 CC combatting viral infections by causing apoptosis of infected cells  
 XX SQ Sequence 28 AA;  
 Query Match 100.0%; Score 102; DB 2; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-10;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 TMGQVGRQLAIIGDDINRRY 20  
 Db 4 TMGQVGRQLAIIGDDINRRY 23  
 RESULT 7  
 AAU77877  
 ID AAU77877 standard; peptide; 28 AA.  
 XX AC AAU77877;  
 XX DT 05-JUN-2002 (first entry)  
 XX DE Bak GD domain region #2 for modulating apoptosis.  
 XX KW GD domain; apoptosis; interaction with Bcl-xL; cell killing function;  
 XX KW bak; cell death regulatory molecule; autoimmune disease; cancer.  
 XX OS Unidentified.  
 XX PN US6221615-B1.  
 XX PD 24-APR-2001.  
 XX PA (AFOP-) APOPTOSIS TECHNOLOGY INC.

PF 25-JAN-1999; 99US-00236385.  
 XX 12-MAY-1995; 95US-00440391.  
 PR 08-AUG-1997; 97US-00908597.  
 XX (AFOP-) APOPTOSIS TECHNOLOGY INC.  
 XX PI Chittenden TD, Lutz RJ;  
 XX DR WPI; 2002-234950/29.  
 XX DR N-PSDB; ABK11177.  
 XX PT Identifying agents (e.g. modulators of apoptosis) capable of modulating  
 XX PT GD domain mediated heterodimerization or homodimerization comprises  
 XX PT carrying out a heterodimerization or homodimerization assay.  
 XX PS Claim 1; Fig 8A; 37pp; English.  
 XX CC The present invention relates to novel peptides, designated GD domains,  
 CC which are capable of modulating apoptosis. The GD domains are essential  
 CC for Bak's interaction with Bcl-xL, and to Bak's cell killing function.  
 CC The GD domains mediate key protein/protein interactions with multiple  
 CC cell death regulatory molecules. Also described are methods of  
 CC identifying agonists or antagonists of GD domains. The methods are useful  
 CC for identifying agents capable of modulating GD domain mediated  
 CC heterodimerisation or homodimerisation. The methods are particularly  
 CC useful in drug screening and design, e.g. for identifying agents for  
 CC treating autoimmune disease or cancer, or for identifying modulators of  
 CC apoptosis. The present sequence represents a GD domain region  
 XX SQ Sequence 28 AA;  
 Query Match 100.0%; Score 102; DB 5; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-10;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 TMGQVGRQLAIIGDDINRRY 20  
 Db 4 TMGQVGRQLAIIGDDINRRY 23  
 RESULT 8  
 ADK14689  
 ID ADK14689 standard; peptide; 28 AA.  
 XX AC ADK14689;  
 XX DT 03-JUN-2004 (first entry)  
 XX DE BCL-2 related gene Bak residues 67-94 seqid 2.  
 XX DE anti-HIV; dermatological; immunosuppressive; antiinflammatory;  
 KW anti-rheumatic; antiarthritic; GD domain peptide; apoptosis;  
 KW protein domain; GD domain; bcl-2 related gene; Bak; cell death;  
 KW immunoreactive protein; degenerative disorder;  
 KW cell proliferation disorder; cell death disorder; autoimmune disease;  
 KW systemic lupus erythematosus; SLE; rheumatoid arthritis;  
 KW acquired immunodeficiency syndrome; AIDS.  
 XX OS Unidentified.  
 XX PN US2004054129-A1.  
 XX PD 18-MAR-2004.  
 XX PF 10-APR-2001; 2001US-00828870.  
 XX PR 12-MAY-1995; 95US-00440391.  
 PR 08-AUG-1997; 97US-00908597.  
 PR 25-JAN-1999; 99US-00236385.  
 XX (AFOP-) APOPTOSIS TECHNOLOGY INC.

PI Chittenden TD, Lutz RJ;  
 XX WPI; 2004-247780/23.  
 DR Novel isolated and purified peptide comprising GD domain, useful for  
 XX treating degenerative disease e.g., rheumatoid arthritis.  
 PT  
 PT  
 PT  
 PS Claim 2; SEQ ID NO 2; 38pp; English.  
 XX  
 CC The invention describes an isolated and purified peptide (I) comprising  
 CC unrecognised protein domain (GD domain) isolated from the bcl-2 related  
 CC gene Bak that can induce cell death. (I) is useful for identifying an  
 CC agent capable of modulating GD domain radiated heterodimerisation or  
 CC homodimerisation. (IV) is useful for screening a cDNA expression library  
 CC for clones comprising DNA inserts encoding immunoreactive proteins  
 CC (claimed). An anti-(I)-antibody, its mimetics, fragments, functional  
 CC equivalents and/or hybrids or its mutants, and a vector comprising a  
 CC polynucleotide encoding (I) are useful as agents for treating  
 CC degenerative disorders including disorders having inappropriate cell  
 CC proliferation or inappropriate cell death. The agents are also useful for  
 CC treating disorders in which a cell is present and/or persists in an  
 CC inappropriate location, and autoimmune disease such as systemic lupus  
 CC erythematosus (SLE) and rheumatoid arthritis. The degenerative disorder  
 CC include acquired immunodeficiency syndrome (AIDS). This is the amino acid  
 CC sequence of Bak residues 67-94, uniquely required for Bak's cell killing  
 CC function.  
 XX  
 SQ Sequence 28 AA;  
 Query Match 100.0%; Score 102; DB 8; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-10;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 TMGQVGRQLAIGDDINRRY 20  
 Db 4 TMGQVGRQLAIGDDINRRY 23  
 RESULT 9  
 ADK14705  
 ID ADK14705 standard; peptide; 28 AA.  
 XX  
 AC ADK14705;  
 XX  
 DT 03-JUN-2004 (first entry)  
 XX  
 DE Bcl-2 related gene Bak residues 67-94 seqid 18.  
 XX  
 KW anti-HIV; dermatological; immunosuppressive; antiinflammatory;  
 KW antirheumatic; antiarthritic; GD domain peptide; apoptosis;  
 KW protein domain; GD domain; bcl-2 related gene; Bak; cell death;  
 KW immunoreactive protein; degenerative disorder;  
 KW cell proliferation disorder; cell death disorder; autoimmune disease;  
 KW systemic lupus erythematosus; SLE; rheumatoid arthritis;  
 KW acquired immunodeficiency syndrome; AIDS.  
 XX  
 OS Unidentified.  
 XX  
 PF US2004054129-A1.  
 XX  
 PN 18-MAR-2004.  
 XX  
 PD 10-APR-2001; 2001US-00828870.  
 XX  
 PR 12-MAY-1995; 95US-00440391.  
 PR 08-AUG-1997; 97US-00908597.  
 PR 25-JAN-1999; 99US-00236385.  
 XX  
 XX (APO-) APOPTOSIS TECHNOLOGY INC.  
 PA Chittenden TD, Lutz RJ;  
 XX WPI; 2004-247780/23.  
 DR

DR N-PSDB; ADK14704.  
 XX  
 PT Novel isolated and purified peptide comprising GD domain, useful for  
 XX treating degenerative disease e.g., rheumatoid arthritis.  
 PT  
 PT  
 PS Disclosure; SEQ ID NO 18; 38pp; English.  
 XX  
 CC The invention describes an isolated and purified peptide (I) comprising  
 CC unrecognised protein domain (GD domain) isolated from the bcl-2 related  
 CC gene Bak that can induce cell death. (I) is useful for identifying an  
 CC agent capable of modulating GD domain radiated heterodimerisation or  
 CC homodimerisation. (IV) is useful for screening a cDNA expression library  
 CC for clones comprising DNA inserts encoding immunoreactive proteins  
 CC (claimed). An anti-(I)-antibody, its mimetics, fragments, functional  
 CC equivalents and/or hybrids or its mutants, and a vector comprising a  
 CC polynucleotide encoding (I) are useful as agents for treating  
 CC degenerative disorders including disorders having inappropriate cell  
 CC proliferation or inappropriate cell death. The agents are also useful for  
 CC treating disorders in which a cell is present and/or persists in an  
 CC inappropriate location, and autoimmune disease such as systemic lupus  
 CC erythematosus (SLE) and rheumatoid arthritis. The degenerative disorder  
 CC include acquired immunodeficiency syndrome (AIDS). This is the amino acid  
 CC sequence of Bak residues 67-94, uniquely required for Bak's cell killing  
 CC function.  
 XX  
 SQ Sequence 28 AA;  
 Query Match 100.0%; Score 102; DB 8; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-10;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 TMGQVGRQLAIGDDINRRY 20  
 Db 4 TMGQVGRQLAIGDDINRRY 23  
 RESULT 10  
 AAU77889  
 ID AAU77889 standard; peptide; 36 AA.  
 XX  
 AC AAU77889;  
 XX  
 DT 05-JUN-2002 (first entry)  
 XX  
 DE Bak GD domain used to identify homologous regions in Bax and Bcl-2.  
 XX  
 KW GD domain; apoptosis; interaction with Bcl-XL; cell killing function;  
 KW bak; cell death regulatory molecule; autoimmune disease; cancer; bax;  
 KW bcl-2.  
 XX  
 OS Unidentified.  
 XX  
 PN US6221615-B1.  
 XX  
 PD 24-APR-2001.  
 XX  
 PF 25-JAN-1999; 99US-00236385.  
 XX  
 PR 12-MAY-1995; 95US-00440391.  
 PR 08-AUG-1997; 97US-00908597.  
 XX  
 XX (APO-) APOPTOSIS TECHNOLOGY INC.  
 PA Chittenden TD, Lutz RJ;  
 XX WPI; 2002-234950/29.  
 DR  
 XX  
 XX Identifying agents (e.g. modulators of apoptosis) capable of modulating  
 XX GD domain mediated heterodimerization or homodimerization comprises  
 XX carrying out a heterodimerization or homodimerization assay.  
 XX  
 PS Example; Fig 5; 37pp; English.  
 XX

CC (claimed): An anti-*Yersinia enterocolitica* monoclonal antibody, and a vector comprising a  
CC equivalents and/or hybrids or its mutants, and a vector comprising a

```

RESULT 13
AAR77876
ID AAR77876 standard; protein; 211 AA.
XX AC AAR77876;
XX AC AAR77876;
XX DT 25-MAR-2003 (revised)
XX DT 21-NOV-1995 (first entry)
XX DE Human Cdn-1.
XX Cdn-1; apoptosis modulator; adoptive immunotherapy; therapy; HIV;
KW autoimmune disease; reperfusion injury; hepatitis, osteoporosis; shock;
KW lymphoma; eczema.
XX OS Homo sapiens.
XX PN WO9515084-A1.
XX PD 08-JUN-1995.
XX PF 30-NOV-1994; 94WO-US013930.
XX PR 30-NOV-1993; 93US-00160067.
XX PR 07-OCT-1994; 94US-00320157.
XX PA (LXRB-) LXR BIOTECHNOLOGY INC.
XX PI Kiefer MC, Barr PJ;
XX WPI; 1995-215106/28.
XX DR N-PSDB; AAQ95492.
XX New nucleic acid sequences encoding Cdn apoptosis modulators - and
PT related vectors, transformed cells, proteins and antibodies, useful for
PT diagnosis and treatment e.g. of HIV infection, reperfusion injury etc.
XX PS Disclosure; Fig 3A-B; 66pp; English.
XX Cdn-1 cDNA was isolated from a human heart cDNA library using a
CC previously isolated clone as probe. Recombinant Cdn-1 was produced in Sf9
CC and human colon adenocarcinoma HT29 cells. Expression of Cdn-1 in WI-L2
CC lymphoblastoid cells resulted in increased cell survival in response to
CC anti-Fas-mediated apoptosis. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX SQ Sequence 211 AA;
Query Match 100.0%; Score 102; DB 2; Length 211;
Best Local Similarity 100.0%; Pred. No. 2.8e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TMGQVGRQLAIGDDINRRY 20
DB 70 TMGQVGRQLAIGDDINRRY 89
RESULT 14
AAR77877
ID AAR77877 standard; protein; 211 AA.
XX AC AAR77877;
XX DT 25-MAR-2003 (revised)
XX DT 21-NOV-1995 (first entry)
XX DE Human Cdn-2.
XX Cdn-2; apoptosis modulator; adoptive immunotherapy; therapy; HIV;
KW autoimmune disease; reperfusion injury; hepatitis, osteoporosis; shock;
KW lymphoma; eczema.

```

```

XX OS Homo sapiens.
XX PN WO9515084-A1.
XX PD 08-JUN-1995.
XX PF 30-NOV-1994; 94WO-US013930.
XX PR 30-NOV-1993; 93US-00160067.
XX PR 07-OCT-1994; 94US-00320157.
XX PA (LXRB-) LXR BIOTECHNOLOGY INC.
XX PI Kiefer MC, Barr PJ;
XX WPI; 1995-215106/28.
XX DR N-PSDB; AAQ95493.
XX New nucleic acid sequences encoding Cdn apoptosis modulators - and
PT related vectors, transformed cells, proteins and antibodies, useful for
PT diagnosis and treatment e.g. of HIV infection, reperfusion injury etc.
XX PS Disclosure; Fig 5D-E; 66pp; English.
XX Cdn-2 cDNA was isold. from a human placental genomic library using a 950
CC bp fragment of Cdn-1 cDNA. Expression of Cdn-2 in mouse progenitor B-cell
CC FL5.12 cells decreased IL-3-induced apoptosis. The Cdn-2 protein
CC displayed 97% amino acid identity with Cdn-1 (AAR77876). (Updated on 25-
CC MAR-2003 to correct PN field.)
XX SQ Sequence 211 AA;
Query Match 100.0%; Score 102; DB 2; Length 211;
Best Local Similarity 100.0%; Pred. No. 2.8e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TMGQVGRQLAIGDDINRRY 20
DB 70 TMGQVGRQLAIGDDINRRY 89
RESULT 15
AAR81451
ID AAR81451 standard; protein; 211 AA.
XX AC AAR81451;
XX DT 02-JUL-1996 (first entry)
XX DE Bcl-Y apoptosis-related protein.
XX KW Bcl-Y; apoptosis; cell proliferation; cell death; diagnosis; therapy.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Domain 188..205
XX FT /label= C-terminal domain
XX FT /note= "putative membrane localisation sequence"
XX PN WO9605232-A1.
XX PD 22-FEB-1996.
XX PF 09-AUG-1995; 95WO-US010103.
XX PR 09-AUG-1994; 94US-00287427.
XX PR 11-OCT-1994; 94US-00321071.
XX PA (IMMU-) IMMUNOGEN INC.
XX PI Chittenden TD;

```



Db |||||  
70 TMGOVGRQLAIGDDINRRY 89

RESULT 18  
AAW79534  
ID AAW79534 standard; protein; 211 AA.

XX AC AAW79534;

XX DT 11-JAN-1999 (first entry)

XX DE Bak polypeptide.

XX KW Bak; bak binding protein; BBP; BBPD-1; BBPD-2; Bcl-2; apoptosis;  
cell death; cancer; lymphoma; neurodegeneration; heart disease;  
cell proliferation; infection; human; therapy; diagnosis.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers  
FT Peptide 103..126  
FT /label= BBPD-1  
FT /note= "Claim 36"

FT Peptide 138..156

FT /label= BBPD-2  
FT /note= "Claim 62"

XX W09841626-A1.

XX PD 24-SEP-1998.

XX PF 03-MAR-1998; 98WO-US004079.

XX PR 20-MAR-1997; 97US-0041328P.

XX PR 09-JAN-1998; 98US-0071097P.

XX PA (LXRB-) LXR BIOTECHNOLOGY INC.

XX PI Kiefer MC, Fitzpatrick PA, Gibson HU, Barr RJ;

XX DR WPI; 1998-521220/44.

XX DR N-PSDB; AAV61498.

XX PT New Bak-binding protein and related nucleic acid, vectors, transformed  
cells and antibodies - are useful for modulation of apoptosis in cancer,  
neuro-degeneration etc., also peptide fragments of Bak that interact with  
the protein.

XX PS Disclosure; Fig 2A-C; 77pp; English.

XX CC This is the amino acid sequence of human Bak, a member of the Bcl-2  
family that is expressed in heart and other tissues, and which is capable  
of either killing cells, or actively protecting cells from apoptosis,  
depending on how it interacts with other cellular proteins. A nucleotide  
sequence (see AAV61498) encoding Bak is provided. The invention relates  
to a novel Bak binding protein (BBP, see AAW79537), the gene encoding BBP  
(see AAV61499), methods for detecting substances that alter the specific  
binding between Bak and BBP, as well as diagnostic and therapeutic  
methods utilising BBP. The invention also encompasses novel Bak-derived  
peptides, designated BBP binding domains (BBPBDs), and novel nucleotides,  
designated bbpd-1 and bbpd-2 encoding the peptides, which are involved  
in the interaction between Bak and BBP, and which have been characterised  
as important death domains of Bak. Modulation of the interaction between  
CC proteins that control apoptosis is a major focal point in the treatment  
of heart disease, viral infection and cancer

XX SQ Sequence 211 AA;

Query Match 100.0%; Score 102; DB 2; Length 211;  
Best Local Similarity 100.0%; Pred. No. 2.8e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TMGOVGRQLAIGDDINRRY 20  
Db |||||  
70 TMGOVGRQLAIGDDINRRY 89

RESULT 19

AAW05433  
ID AAW05433 standard; peptide; 211 AA.

XX AC AAW05433;

XX DT 02-JUL-1999 (first entry)

XX DE Human BAK protein sequence.

XX KW BH3 domain; cell death agonist; bcl homology domain; BCL-2 family;  
apoptosis promoter; cancer cell; virus infected cell; inflammation;  
autocatalytic producing cell; cancer; lymphoproliferative condition;  
arthritis; autoimmune disease; therapy.

XX OS Homo sapiens.

XX PN W09916787-A1.

XX PD 08-APR-1999.

XX PF 22-SEP-1998; 98WO-US019765.

XX PR 26-SEP-1997; 97US-0060133P.

XX PR 07-OCT-1997; 97US-00946039.

XX PA (UNIW ) UNIV WASHINGTON.

XX PI Korsmeyer SJ;

XX DR WPI; 1999-255058/21.

XX PT Bcl homology domain 3 polypeptide.

XX PS Disclosure; Fig 21b; 104pp; English.

XX CC This sequence represents the human BAK protein. The invention relates to  
a bcl homology domain 3 (BH3 domain), derived from a proapoptotic member  
of the BCL-2 family. The BH3 polypeptide can be used in a method for  
promoting apoptosis in a target cell, especially where the cell is a  
cancer cell, a virus infected cell or an antibody producing cell. The  
BH3 polypeptide can be used in therapeutic compositions for treating  
disease including cancer, other lymphoproliferative conditions,  
arthritis, inflammation, and autoimmune diseases, which may result from  
the down regulation of cell death regulation

XX SQ Sequence 211 AA;

Query Match 100.0%; Score 102; DB 2; Length 211;  
Best Local Similarity 100.0%; Pred. No. 2.8e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TMGOVGRQLAIGDDINRRY 20  
Db |||||  
70 TMGOVGRQLAIGDDINRRY 89

RESULT 20

ABB82374

ID ABB82374 standard; protein; 211 AA.

XX AC ABB82374;

XX DT 08-JAN-2003 (first entry)

XX DE Human BAK protein sequence.

XX KW BAK; MILL; cytostatic; neuroprotective; nootropic; cerebroprotective;

KW apoptosis; human.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO200274908-A2.  
 XX  
 PD 26-SEP-2002.  
 XX  
 PF 04-MAR-2002; 2002WO-US006757.  
 XX  
 PR 02-MAR-2001; 2001US-0273091P.  
 XX  
 FA (MDSB-) MDS PROTEOMICS INC.  
 XX  
 PI Mcfadden G, Moran MF;  
 XX  
 XX WPI; 2002-740855/80.  
 DR  
 XX Identifying agents which may be potentially pro-apoptotic or anti-  
 XX apoptotic for treating acute and chronic neurodegenerative diseases,  
 PT comprises determining the effect of the test agent on complexes of BAK  
 PT and/or M1L1 proteins.  
 XX  
 XX Disclosure; Fig 11; 83pp; English.  
 PS  
 XX The invention relates to identifying agents which may be potentially pro-  
 CC apoptotic or anti-apoptotic which involves determining the effect of a  
 CC test agent on the complexes of BAK and/or M1L1 proteins. The methods are  
 CC useful for identifying agents which may be potentially pro-apoptotic or  
 CC anti-apoptotic and for identifying M1L1-interacting polypeptides, and in  
 CC conducting a target or drug discovery system. The methods are useful for  
 CC identifying agents capable of inhibiting M1L1 activity or which can mimic  
 CC the activity of M1L1 by inhibiting the activity of BAK and which are  
 CC therefore anti-apoptotic agents. Agents identified by the method as  
 CC involved in regulation of apoptosis may be used in the development of  
 CC therapeutic agents and methods, and drug screening assays, and in  
 CC increasing the sensitivity of cancer cells to chemotherapeutic treatment.  
 CC Therapeutic applications of apoptosis manipulation include treatment of  
 CC acute and chronic neurodegenerative diseases, e.g. stroke, Alzheimer's or  
 CC Huntington's disease by drugs, and sensitization of cancer cells for drug  
 CC /radiation-induced apoptosis by modulation of survival signals and viral  
 CC transfer of apoptosis promoting genes. The present sequence represents a  
 CC human BAK protein  
 XX  
 SQ Sequence 211 AA;  
 Query Match 100.0%; Score 102; DB 5; Length 211;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 TMGQVGRQLAIIIGDDINRRY 20  
 |||||  
 DB 70 TMGQVGRQLAIIIGDDINRRY 89  
 |||||  
 RESULT 21  
 AAEE37655  
 ID AAEE37655 standard; protein; 211 AA.  
 XX  
 AC AAEE37655;  
 XX  
 XX 27-AUG-2003 (first entry)  
 DT  
 DE Bcl2 related protein #6.  
 XX  
 XX Bcl2 related protein; growth; protein expression.  
 KW  
 XX Unidentified.  
 OS  
 XX WO2003040374-A1.  
 FN  
 XX 15-MAY-2003.  
 PD  
 XX

PF 02-NOV-2001; 2001WO-US045553.  
 XX  
 PR 02-NOV-2001; 2001WO-US045553.  
 XX  
 FA (CENZ ) CENTOCOR INC.  
 XX  
 PI Lee C, Ly C, Moore G, Shi X;  
 XX  
 XX WPI; 2003-441576/41.  
 DR  
 XX New protein expression enhancing Bcl2 related nucleic acid for producing  
 PT commercially useful amounts of expressed protein, comprises a nucleic  
 PT acid that encodes an expressible protein or at least one Bcl2 related  
 PT protein.  
 XX  
 XX Disclosure; Page 52-53; 64pp; English.  
 PS  
 XX The invention relates to methods and compositions for enhanced protein  
 CC expression and/or growth of cultured cells using co-transcription of at  
 CC least one Bcl2 related protein encoding nucleic acid molecules. The  
 CC invention is useful in providing enhanced growth of and/or protein  
 CC production from cultured mammalian host cells used for the production of  
 CC commercially useful amounts of expressed protein. The present sequence is  
 CC Bcl2 related protein  
 XX  
 SQ Sequence 211 AA;  
 Query Match 100.0%; Score 102; DB 6; Length 211;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 TMGQVGRQLAIIIGDDINRRY 20  
 |||||  
 DB 70 TMGQVGRQLAIIIGDDINRRY 89  
 |||||  
 RESULT 22  
 ABR47397  
 ID ABR47397 standard; protein; 211 AA.  
 XX  
 AC ABR47397;  
 XX  
 XX 12-JUN-2003 (first entry)  
 DT  
 XX  
 DE Breast cancer associated protein sequence SEQ ID NO:25.  
 XX  
 DE Human; breast cancer; cytostatic; gene therapy.  
 KW  
 XX Homo sapiens.  
 OS  
 XX WO2003004989-A2.  
 FN  
 XX 16-JAN-2003.  
 PD  
 XX  
 XX 21-JUN-2002; 2002WO-US019669.  
 PF  
 XX 21-JUN-2001; 2001US-0299887P.  
 PR  
 PR 27-JUN-2001; 2001US-0301572P.  
 PR  
 PR 18-JUL-2001; 2001US-0306501P.  
 PR  
 PR 25-SEP-2001; 2001US-0325002P.  
 PR  
 PR 05-MAR-2002; 2002US-0362585P.  
 PR  
 PR 14-MAY-2002; 2002US-0380391P.  
 PR  
 XX (MILL-) MILLENIUM PHARM INC.  
 PA  
 XX Lillie J, Gannavarapu M, Glatt K, Hoersht S, Kamatkar S;  
 PI Mertens M, Monahan JE, Myer V, Wang Y, Xu Y, Zhao X, Meyers RE;  
 PI Bast RC, Hortobagyi GN, Pusztai L, Meric F, Sahin A, Mills GB;  
 XX  
 XX WPI; 2003-210381/20.  
 DR  
 DR N-PSDB; ACC50088.  
 XX  
 XX Breast cancer diagnosis or treatment by comparing the level of expression  
 PT



PT of a marker in a patient sample with that in the control non-breast  
PT cancer sample.  
XX  
PS Claim 1; SEQ ID NO 25; 128pp; English.  
XX  
CC The present invention describes a method for assessing whether a patient  
CC is afflicted with breast cancer. The method comprises comparing the level  
CC of expression of a marker (gene/polypeptide see ACC50076 to ACC50334 and  
CC ABR47386 to ABR47632) in a patient sample and the normal level of  
CC expression of the marker in a control non-breast cancer sample, where a  
CC significant increase in the level of expression of the marker in the  
CC patient sample and the normal level is an indication that the patient is  
CC afflicted with breast cancer. The breast cancer associated sequences from  
CC the present invention have cytostatic activities and can be used in gene  
CC therapy. The method is useful for diagnosing and treating breast cancer.  
CC N.B. The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 211 AA;

Query Match 100.0%; Score 102; DB 6; Length 211;  
Best Local Similarity 100.0%; Pred. No. 2.8e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TMGQVGRQLAIIIGDDINRRY 20  
DB 70 TMGQVGRQLAIIIGDDINRRY 89

RESULT 23  
ADD93300  
ID ADD93300 standard; protein; 211 AA.  
XX  
AC ADD93300;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Human pro-apoptotic protein Bak.  
XX  
KW Human; Bak; cytostatic; apoptosis.  
XX  
OS Homo sapiens.  
XX  
PN WO2003062828-A2.  
XX  
PD 31-JUL-2003.  
XX  
PF 17-JAN-2003; 2003WO-GB000162.  
XX  
PR 17-JAN-2002; 2002GB-00000971.  
XX  
PA (UYMA-) UNIV VICTORIA MANCHESTER.  
XX  
PI Griffiths GJ;  
XX  
DR WPI; 2003-748015/70.  
XX  
PT Determining potential effect of chemotherapeutic agents, useful for  
PT treating cancer, from their ability to induce conformational change in  
PT Bak protein.  
XX  
PS Disclosure; SEQ ID NO 1; 16pp; English.  
XX  
CC The present sequence is the protein sequence of the human pro-apoptotic  
CC protein, Bak. A conformational change in the Bak protein is used in the  
CC method of the invention for determining the potential effectiveness of a  
CC chemotherapeutic compound for treating cancerous cells in a human or  
CC animal patient. The method involves: (i) exposing a sample of the  
CC cancerous cells taken from the patient to a chemotherapeutic compound, or  
CC combination of compounds; and (ii) assaying for a conformational change  
CC in the Bak protein of the cells. The conformational change is preferably  
CC determined at the N-terminus of Bak or in its BHI domain, particularly

CC using a specific binding partner, such as an antibody, for the  
CC conformationally altered protein. Conformational change in Bak is a very  
CC early (and general) indicator of commitment to apoptosis, occurring  
CC before caspase activation, nuclear condensation or cellular blebbing, and  
CC is caused by agents that induce apoptosis by different mechanisms.  
CC Detecting commitment to apoptosis is a more accurate indicator of  
CC activity than cell death and the present method is quicker and simpler  
CC than known clonogenic assays.  
XX  
SQ Sequence 211 AA;

Query Match 100.0%; Score 102; DB 7; Length 211;  
Best Local Similarity 100.0%; Pred. No. 2.8e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TMGQVGRQLAIIIGDDINRRY 20  
DB 70 TMGQVGRQLAIIIGDDINRRY 89

RESULT 24  
ADF60830  
ID ADF60830 standard; protein; 211 AA.  
XX  
AC ADF60830;  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Human Bak #SEQ ID 1.  
XX  
KW Chemotherapeutic; anti-apoptotic; Bak; Bcl-2; Bcl-XL; cancer; human.  
XX  
OS Homo sapiens.  
XX  
PN WO2003062829-A2.  
XX  
PD 31-JUL-2003.  
XX  
PF 17-JAN-2003; 2003WO-GB000185.  
XX  
PR 17-JAN-2002; 2002GB-00000970.  
XX  
PA (UYMA-) UNIV VICTORIA MANCHESTER.  
XX  
PI Griffiths GJ;  
XX  
DR WPI; 2003-902664/82.  
XX  
PT Detecting or screening for chemotherapeutic activity, useful for treating  
PT cancer, from induction of modifications in Bak protein in cells over  
PT expressing anti-apoptotic protein.  
XX  
PS Disclosure; Page 3; 32pp; English.  
XX  
CC The invention relates to a method for detecting a chemotherapeutic  
CC activity in a compound other than an etoposide, or in a combination of  
CC compounds. In the method of the invention, a cell that over expresses an  
CC anti-apoptotic protein is treated with at least one compound, and any  
CC change in the conformation of cellular Bak, indicative of  
CC chemotherapeutic activity, is detected. The anti-apoptotic protein is Bcl  
CC -2 or Bcl-XL, and is over expressed by transfecting the cells with a  
CC pcDNA3.1 vector that contains the anti-apoptotic-expressing sequence  
CC under control of the cytomegalovirus promoter. The method of the  
CC invention is used to identify, or screen for, chemotherapeutic agents for  
CC the treatment of cancer. The current sequence represents the human Bak  
CC amino acid sequence.  
XX  
SQ Sequence 211 AA;

Query Match 100.0%; Score 102; DB 7; Length 211;  
Best Local Similarity 100.0%; Pred. No. 2.8e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
OY 1 TMGQVGRQLAIGDDINRRY 20
DB 70 TMGQVGRQLAIGDDINRRY 89

RESULT 25
ADL69726
ID ADL69726 standard; protein; 211 AA.
XX
AC ADL69726;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human Bcl2 related protein #6.
XX
KW Bcl2 related protein; therapeutic protein; human.
OS
OS Homo sapiens.
XX
PN US2004043028-A1.
XX
PD 04-MAR-2004.
XX
PF 02-NOV-2001; 2001US-00003632.
XX
PR 02-NOV-2001; 2001US-00003632.
XX
PA (LEEC/) LEE C.
PA (SHIX/) SHI X.
PA (LYCC/) LY C.
PA (MOOR/) MOORE G.
XX
PI Lee C, Shi X, Ly C, Moore G;
XX
XX WPI; 2004-225672/21.
XX
XX New Bcl2 encoding nucleic acids for enhancing growth and/or production of
XX therapeutic or diagnostic proteins from cultured mammalian host cells.
XX
XX Disclosure; SEQ ID NO 6; 42pp; English.
XX
XX The invention relates to a protein expression enhancing Bcl2 related
XX nucleic acid comprising a first nucleic acid encoding at least one
XX expressible protein and a second nucleic acid encoding at least one Bcl2
XX related protein, where expression of the expressible protein is enhanced
XX by transcription or translation of the second nucleic acid. The
XX composition and methods are useful for enhancing growth and/or production
XX of therapeutic or diagnostic proteins from cultured mammalian host cells.
XX The present sequence is human Bcl2 related protein.
XX
XX Sequence 211 AA;

Query Match 100.0%; Score 102; DB 8; Length 211;
Best Local Similarity 100.0%; Pred. No. 2.8e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TMGQVGRQLAIGDDINRRY 20
DB 70 TMGQVGRQLAIGDDINRRY 89

RESULT 26
ADP04114
ID ADP04114 standard; protein; 211 AA.
XX
AC ADP04114;
XX
DT 09-SEP-2004 (first entry)
XX
DE Human colon specific protein SEQ ID NO:95.
XX
KW human; colon specific nucleic acid; CSNA; colon specific protein; CSP;
XX cytostatic; vaccine; gene therapy; colon cancer.
```

```
XX Homo sapiens.
OS
XX WO2004050858-A2.
PN
XX 17-JUN-2004.
PD
XX 04-DEC-2003; 2003WO-US038808.
PF
XX 04-DEC-2002; 2002US-0431133P.
PR
XX (DIAD-) DIADEXUS INC.
PA
XX Macina RA, Turner LR, Sun Y, Rodriguez M, Burcham TS;
PI
XX WPI; 2004-480622/45.
PD
XX Novel colon specific protein derived from normal and neoplastic colon
PT cell, useful as vaccine in treating colon cancer and in identifying,
PT diagnosing, monitoring, staging, imaging colon cancer and non-cancerous
PT disease state in colon.
XX
XX Claim 12; SEQ ID NO 95; 655pp; English.
XX
XX The invention relates to a novel colon specific protein (CSP) (I), and
XX the nucleic acid encoding it. A CSP of the invention has cytostatic
XX activity, and may have use in a vaccine, and in gene therapy. The CSP is
XX useful for determining the presence of a colon specific protein in a
XX sample. The nucleic acid encoding the CSP is useful for determining the
XX presence of a colon specific nucleic acid (CSNA) in a sample. The CSP and
XX CSNA are useful for diagnosing or monitoring the presence and metastases
XX of colon cancer in a patient. The method of administering a composition
XX comprising a CSP or CSNA is useful for treating a patient with colon
XX cancer. The CSP and CSNA are useful as vaccine for treating colon cancer
XX and non-cancerous disease states in colon. The present sequence
XX represents a CSP of the invention.
XX
XX Sequence 211 AA;

Query Match 100.0%; Score 102; DB 8; Length 211;
Best Local Similarity 100.0%; Pred. No. 2.8e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TMGQVGRQLAIGDDINRRY 20
DB 70 TMGQVGRQLAIGDDINRRY 89

Search completed: January 26, 2005, 00:55:12
Job time : 172 secs
```

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 25, 2005, 10:10:46 ; Search time 97.5 Seconds  
(without alignments)  
74.111 Million cell updates/sec

Title: US-09-828-870-36

Perfect score: 102

Sequence: 1 TMQVGRQLAIIGDDINRRY 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*  
17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*  
19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	102	100.0	20	11 US-09-828-870-36	Sequence 36, Appl
2	102	100.0	28	11 US-09-828-870-2	Sequence 2, Appli
3	102	100.0	28	11 US-09-828-870-18	Sequence 18, Appl
4	102	100.0	36	11 US-09-828-870-14	Sequence 14, Appl
5	102	100.0	210	14 US-10-101-482-22	Sequence 22, Appl
6	102	100.0	211	14 US-10-101-482-7	Sequence 7, Appli
7	102	100.0	211	14 US-10-101-482-9	Sequence 9, Appli
8	102	100.0	211	14 US-10-101-482-10	Sequence 10, Appl
9	102	100.0	211	14 US-10-101-482-11	Sequence 11, Appl
10	102	100.0	211	14 US-10-189-294-2	Sequence 2, Appli
11	102	100.0	211	14 US-10-177-293-25	Sequence 25, Appl
12	102	100.0	211	15 US-10-003-632C-6	Sequence 6, Appli
13	102	100.0	211	17 US-10-825-282-34	Sequence 34, Appl

14 97 95.1 19 11 US-09-828-870-35 Sequence 35, Appl  
15 97 95.1 117 14 US-10-189-294-4 Sequence 0, Appli  
16 90 88.2 28 14 US-10-092-750-152 Sequence 152, App  
17 86 84.3 31 11 US-09-828-870-3 Sequence 3, Appli  
18 86 84.3 31 11 US-09-828-870-16 Sequence 16, Appl  
19 85 83.3 17 14 US-10-092-750-240 Sequence 240, App  
20 85 83.3 18 14 US-10-092-750-2 Sequence 41, Appl  
21 85 83.3 18 14 US-10-092-750-41 Sequence 41, Appl  
22 80 78.4 16 10 US-09-840-085-73 Sequence 73, Appli  
23 80 78.4 16 14 US-10-158-769-3 Sequence 3, Appli  
24 80 78.4 16 14 US-10-059-261-240 Sequence 240, App  
25 80 78.4 16 17 US-10-729-156-9 Sequence 9, Appli  
26 80 78.4 16 17 US-10-627-649-240 Sequence 240, App  
27 80 78.4 19 14 US-10-196-080-2 Sequence 2, Appli  
28 74 72.5 15 9 US-09-738-396-11 Sequence 11, Appli  
29 74 72.5 15 11 US-09-828-870-10 Sequence 10, Appl  
30 74 72.5 15 11 US-09-828-870-20 Sequence 20, Appl  
31 74 72.5 15 11 US-09-828-870-37 Sequence 37, Appl  
32 57 67.6 15 11 US-09-828-870-38 Sequence 38, Appl  
33 57 55.9 24 9 US-09-682-667-16 Sequence 16, Appl  
34 57 55.9 24 17 US-10-870-197-16 Sequence 16, Appl  
35 53 52.0 15 10 US-09-840-085-24 Sequence 24, Appl  
36 50 49.0 226 15 US-10-425-114-56560 Sequence 56560, A  
37 50 49.0 444 17 US-10-425-115-261716 Sequence 261716, A  
38 48 47.1 208 14 US-10-195-144-49 Sequence 49, Appl  
39 48 47.1 208 14 US-10-345-072-49 Sequence 49, Appl  
40 47 46.1 15 9 US-09-912-599-15 Sequence 15, Appl  
41 47 46.1 165 9 US-09-912-599-9 Sequence 9, Appli  
42 47 46.1 195 9 US-09-912-598-8 Sequence 8, Appli  
43 46 45.1 15 10 US-09-840-085-25 Sequence 25, Appl  
44 46 45.1 720 15 US-10-282-122A-72880 Sequence 72880, A  
45 46 45.1 833 15 US-10-282-122A-75511 Sequence 75511, A

#### ALIGNMENTS

RESULT 1  
US-09-828-870-36  
; Sequence 36, Application US/09828870  
; Publication No. US20040054129A1  
; GENERAL INFORMATION:  
; APPLICANT: CHITTENDEN, Thomas D.; and  
; LUTZ, Robert J.  
; TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH  
; MODULATE APOPTOSIS  
; NUMBER OF SEQUENCES: 41  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hale and Dorr  
; STREET: 1455 Pennsylvania Avenue, N.W.  
; CITY: Washington  
; STATE: D.C.  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/09/828,870  
; APPLICATION NUMBER: US/09/828,870  
; FILING DATE: 10-Apr-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/236,385  
; FILING DATE: 25-JANUARY-1999  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WIXON, HENRY N.  
; REGISTRATION NUMBER: 32,073  
; (C) ATTORNEY DOCKET NO. 104322.147CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-942-8400  
; TELEFAX: 202-942-8484  
; INFORMATION FOR SEQ ID NO: 36

SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 36  
US-09-828-870-36

Query Match 100.0%; Score 102; DB 11; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TMQVGRQLAIGDDINRRY 20  
DB 1 TMQVGRQLAIGDDINRRY 20

## RESULT 2

US-09-828-870-2  
Sequence 2, Application US/09828870  
Publication No. US20040054129A1

GENERAL INFORMATION:  
APPLICANT: CHITTENDEN, Thomas D.; and  
LUTZ, Robert J.

TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH  
MODULATE APOPTOSIS

NUMBER OF SEQUENCES: 41

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hale and Dorr  
STREET: 1455 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: D.C.  
ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA: US/09/828, 870  
FILING DATE: 10-Apr-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/236,385

FILING DATE: 25-JANUARY-1999

ATTORNEY/AGENT INFORMATION:

NAME: WIXON, HENRY N.

REGISTRATION NUMBER: 32,073

TELECOMMUNICATION INFORMATION:  
(C) ATTORNEY DOCKET NO. 104322.147CIP

TELEPHONE: 202-942-8400

TELEFAX: 202-942-8484

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 28 amino acid

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-828-870-2

Query Match 100.0%; Score 102; DB 11; Length 28;  
Best Local Similarity 100.0%; Pred. No. 1.6e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TMQVGRQLAIGDDINRRY 20  
DB 4 TMQVGRQLAIGDDINRRY 23

## RESULT 3

US-09-828-870-18

Sequence 18, Application US/09828870

Publication No. US20040054129A1  
GENERAL INFORMATION:  
APPLICANT: CHITTENDEN, Thomas D.; and  
LUTZ, Robert J.  
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH  
MODULATE APOPTOSIS  
NUMBER OF SEQUENCES: 41  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr  
STREET: 1455 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: D.C.  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA: US/09/828, 870  
FILING DATE: 10-Apr-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/236,385  
FILING DATE: 25-JANUARY-1999  
ATTORNEY/AGENT INFORMATION:  
NAME: WIXON, HENRY N.  
REGISTRATION NUMBER: 32,073  
TELECOMMUNICATION INFORMATION:  
(C) ATTORNEY DOCKET NO. 104322.147CIP

TELEPHONE: 202-942-8400

TELEFAX: 202-942-8484

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:

LENGTH: 28 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 18:

US-09-828-870-18

Query Match 100.0%; Score 102; DB 11; Length 28;  
Best Local Similarity 100.0%; Pred. No. 1.6e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TMQVGRQLAIGDDINRRY 20

DB 4 TMQVGRQLAIGDDINRRY 23

## RESULT 4

US-09-828-870-14

Sequence 14, Application US/09828870

Publication No. US20040054129A1

GENERAL INFORMATION:

APPLICANT: CHITTENDEN, Thomas D.; and

LUTZ, Robert J.

TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH

MODULATE APOPTOSIS

NUMBER OF SEQUENCES: 41

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hale and Dorr

STREET: 1455 Pennsylvania Avenue, N.W.

CITY: Washington

STATE: D.C.

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/828, 870

;  
; FILING DATE: 10-Apr-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/236,385  
; FILING DATE: 25-JANUARY-1999  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WIXON, HENRY N.  
; REGISTRATION NUMBER: 32,073  
; (C) ATTORNEY DOCKET NO. 1043322.147CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-942-8400  
; TELEFAX: 202-942-8484  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 36 base pairs  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:  
US-09-828-870-14  
;  
; Query Match 100.0%; Score 102; DB 11; Length 36;  
; Best Local Similarity 100.0%; Pred. No. 2.1e-09;  
; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
;  
QY 1 TMQGVGRQLAIIIGDDINRRY 20  
Db 6 TMQGVGRQLAIIIGDDINRRY 25  
;  
RESULT 5  
US-10-101-482-22  
; Sequence 22, Application US/10101482  
; Publication No. US20030008837A1  
; GENERAL INFORMATION:  
; APPLICANT: KIEFER, MICHAEL C.  
; BARR, PHILIP J.  
; TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA  
; ENCODING THE PROTEINS AND METHODS OF USE THEREOF  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/101,482  
; FILING DATE: 18-Mar-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/320,157  
; FILING DATE: 07-OCT-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: LEHNHARDT, SUSAN K.  
; REGISTRATION NUMBER: 33,943  
; REFERENCE/DOCKET NUMBER: 23647-20007.20  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 813-5600  
; TELEFAX: (415) 494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 22:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 210 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
;  
; Query Match 100.0%; Score 102; DB 11; Length 36;  
; Best Local Similarity 100.0%; Pred. No. 2.1e-09;  
; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
;  
QY 1 TMQGVGRQLAIIIGDDINRRY 20  
Db 6 TMQGVGRQLAIIIGDDINRRY 25  
;  
RESULT 6  
US-10-101-482-7  
; Sequence 7, Application US/10101482  
; Publication No. US20030008837A1  
; GENERAL INFORMATION:  
; APPLICANT: KIEFER, MICHAEL C.  
; BARR, PHILIP J.  
; TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA  
; ENCODING THE PROTEINS AND METHODS OF USE THEREOF  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/101,482  
; FILING DATE: 18-Mar-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/320,157  
; FILING DATE: 07-OCT-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: LEHNHARDT, SUSAN K.  
; REGISTRATION NUMBER: 33,943  
; REFERENCE/DOCKET NUMBER: 23647-20007.20  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 813-5600  
; TELEFAX: (415) 494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 211 amino acids  
; TYPE: amino acid  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
US-10-101-482-7  
;  
; Query Match 100.0%; Score 102; DB 14; Length 211;  
; Best Local Similarity 100.0%; Pred. No. 1.5e-08;  
; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
;  
QY 1 TMQGVGRQLAIIIGDDINRRY 20  
Db 70 TMQGVGRQLAIIIGDDINRRY 89  
;  
RESULT 7  
US-10-101-482-9  
; Sequence 9, Application US/10101482  
; Publication No. US20030008837A1  
; GENERAL INFORMATION:  
; APPLICANT: KIEFER, MICHAEL C.

;  
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:  
US-10-101-482-22  
;  
; Query Match 100.0%; Score 102; DB 14; Length 210;  
; Best Local Similarity 100.0%; Pred. No. 1.4e-08;  
; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
;  
QY 1 TMQGVGRQLAIIIGDDINRRY 20  
Db 70 TMQGVGRQLAIIIGDDINRRY 89  
;  
RESULT 6  
US-10-101-482-7  
; Sequence 7, Application US/10101482  
; Publication No. US20030008837A1  
; GENERAL INFORMATION:  
; APPLICANT: KIEFER, MICHAEL C.  
; BARR, PHILIP J.  
; TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA  
; ENCODING THE PROTEINS AND METHODS OF USE THEREOF  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/101,482  
; FILING DATE: 18-Mar-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/320,157  
; FILING DATE: 07-OCT-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: LEHNHARDT, SUSAN K.  
; REGISTRATION NUMBER: 33,943  
; REFERENCE/DOCKET NUMBER: 23647-20007.20  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 813-5600  
; TELEFAX: (415) 494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 211 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
US-10-101-482-7  
;  
; Query Match 100.0%; Score 102; DB 14; Length 211;  
; Best Local Similarity 100.0%; Pred. No. 1.5e-08;  
; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
;  
QY 1 TMQGVGRQLAIIIGDDINRRY 20  
Db 70 TMQGVGRQLAIIIGDDINRRY 89  
;  
RESULT 7  
US-10-101-482-9  
; Sequence 9, Application US/10101482  
; Publication No. US20030008837A1  
; GENERAL INFORMATION:  
; APPLICANT: KIEFER, MICHAEL C.

```
;
; BARR, PHILIP J.
; TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
; ENCODING THE PROTEINS AND METHODS OF USE THEREOF
;
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/101,482
; FILING DATE: 18-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/320,157
; FILING DATE: 07-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: LEHNHARDT, SUSAN K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20007.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 211 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-101-482-9
Query Match 100.0%; Score 102; DB 14; Length 211;
Best Local Similarity 100.0%; Pred. No. 1.5e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TMGVGRLAIIGDDINRRY 20
Db 70 TMGVGRLAIIGDDINRRY 89

RESULT 8
US-10-101-482-10
; Sequence 10, Application US/10101482
; Publication No. US20030008837A1
; GENERAL INFORMATION:
; APPLICANT: KIEFER, MICHAEL C.
; BARR, PHILIP J.
; TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
; ENCODING THE PROTEINS AND METHODS OF USE THEREOF
;
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/101,482
; FILING DATE: 18-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/320,157
; FILING DATE: 07-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: LEHNHARDT, SUSAN K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20007.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 211 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; APPLICATION NUMBER: US/10/101,482
```

```
;
; FILING DATE: 18-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/320,157
; FILING DATE: 07-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: LEHNHARDT, SUSAN K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20007.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 211 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-101-482-10
Query Match 100.0%; Score 102; DB 14; Length 211;
Best Local Similarity 100.0%; Pred. No. 1.5e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TMGVGRLAIIGDDINRRY 20
Db 70 TMGVGRLAIIGDDINRRY 89

RESULT 9
US-10-101-482-11
; Sequence 11, Application US/10101482
; Publication No. US20030008837A1
; GENERAL INFORMATION:
; APPLICANT: KIEFER, MICHAEL C.
; BARR, PHILIP J.
; TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
; ENCODING THE PROTEINS AND METHODS OF USE THEREOF
;
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/101,482
; FILING DATE: 18-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/320,157
; FILING DATE: 07-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: LEHNHARDT, SUSAN K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20007.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 211 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
```

```
;
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-101-482-11

Query Match      100.0%; Score 102; DB 14; Length 211;
Best Local Similarity 100.0%; Pred. No. 1.5e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TMQGVGRQLAIGDDINRRY 20
Db 70 TMQGVGRQLAIGDDINRRY 89

RESULT 10
US-10-189-294-2
; Sequence 2, Application US/10189294
; Publication No. US20030060615A1
; GENERAL INFORMATION:
; APPLICANT: Kiefer, Michael C.
; Gibson, Helen L.
; Fitzpatrick, Paul A.
; Barr, Philip J.
; TITLE OF INVENTION: A NOVEL BAK BINDING PROTEIN, DNA
; ENCODING THE PROTEIN, AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWN, THERESA A.
; STREET: 1560 Broadway, Suite 1200
; CITY: Denver
; STATE: CO
; COUNTRY: USA
; ZIP: 80202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/189,294
; FILING DATE: 01-Jul-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/381,488
; FILING DATE: 11-Feb-2000
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWN, THERESA A.
; REGISTRATION NUMBER: 32,547
; REFERENCE/DOCKET NUMBER: 4147-15-PUS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 211 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-189-294-2

Query Match      100.0%; Score 102; DB 14; Length 211;
Best Local Similarity 100.0%; Pred. No. 1.5e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TMQGVGRQLAIGDDINRRY 20
Db 70 TMQGVGRQLAIGDDINRRY 89

RESULT 11
US-10-177-293-25
; Sequence 25, Application US/10177293
; Publication No. US20030124128A1
```

```
;
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; Glatt, Karen
; Zhao, Xumei
; APPLICANT: Gannavarpu, Manjula
; Kamatkar, Shubhangi
; Mertens, Maureen
; Myer, Vic
; APPLICANT: Wang, Youzhen
; Xu, Yongyao
; APPLICANT: Hoersch, Sebastian
; Monahan, John
; APPLICANT: Meyers, Rachel E.
; Bast Jr., Robert C.
; APPLICANT: Hortobagyi, Gabriel N.
; Pusztai, Lajos
; APPLICANT: Meric, Funda
; APPLICANT: Sahin, Aysegul
; APPLICANT: Mills, Gordon B.
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
; PREVENTION, AND THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-038
; CURRENT APPLICATION NUMBER: US/10/177,293
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/299,887
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/301,572
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/306,501
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/325,002
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/362,585
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/xxx,xxx
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-177-293-25

Query Match      100.0%; Score 102; DB 14; Length 211;
Best Local Similarity 100.0%; Pred. No. 1.5e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TMQGVGRQLAIGDDINRRY 20
Db 70 TMQGVGRQLAIGDDINRRY 89

RESULT 12
US-10-003-632C-6
; Sequence 6, Application US/10003632C
; Publication No. US20040043028A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Chichang; Ly, Celia; Moore, Gordon; Chi, Xianmei
; TITLE OF INVENTION: Methods and Compositions for Enhanced Protein Expression and/or
; Transcription of a Bcl2 Encoding Nuclei
; FILE REFERENCE: CEN0269
; CURRENT APPLICATION NUMBER: US/10/003,632C
; CURRENT FILING DATE: 2001-11-02
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin Ver 3.1
; SEQ ID NO 6
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-003-632C-6

Query Match      100.0%; Score 102; DB 15; Length 211;
```

Best Local Similarity 100.0%; Pred. No. 1.5e-08; Indels 0; Gaps 0;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TMQVGRQLAIGDDINRRY 20  
Db 70 TMQVGRQLAIGDDINRRY 89

RESULT 13  
US-10-825-282-34  
; Sequence 34, Application US/10825282  
; Publication No. US20040224389A1  
; GENERAL INFORMATION:  
; APPLICANT: 3921-1-1-1  
; TITLE OF INVENTION: VIRAL VECTORS ENCODING APOPTOSIS-INDUCING PROTEINS AND  
; METHODS FOR MAKING AND USING THE SAME  
; FILE REFERENCE: 3921-1-1-1  
; CURRENT APPLICATION NUMBER: US/10/825,282  
; CURRENT FILING DATE: 2004-04-14  
; PRIOR APPLICATION NUMBER: US/09/456,357  
; PRIOR FILING DATE: 1999-12-08  
; PRIOR APPLICATION NUMBER: 60/134,416  
; PRIOR FILING DATE: 1999-05-17  
; PRIOR APPLICATION NUMBER: 09/087,195  
; PRIOR FILING DATE: 1998-05-29  
; PRIOR APPLICATION NUMBER: 08/378,507  
; PRIOR FILING DATE: 1995-01-26  
; PRIOR APPLICATION NUMBER: 08/250,478  
; PRIOR FILING DATE: 1994-05-27  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 34  
; LENGTH: 211  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-825-282-34

Query Match 100.0%; Score 102; DB 17; Length 211;  
Best Local Similarity 100.0%; Pred. No. 1.5e-08;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TMQVGRQLAIGDDINRRY 20  
Db 70 TMQVGRQLAIGDDINRRY 89

RESULT 14  
US-09-828-870-35  
; Sequence 35, Application US/09828870  
; Publication No. US20040054129A1  
; GENERAL INFORMATION:  
; APPLICANT: CHITTENDEN, Thomas D.; and  
; LUTZ, Robert J.  
; TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH  
; MODULATE APOPTOSIS  
; NUMBER OF SEQUENCES: 41  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hale and Dorr  
; STREET: 1455 Pennsylvania Avenue, N.W.  
; CITY: Washington  
; STATE: D.C.  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/828,870  
; FILING DATE: 10-Apr-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/236,385

FILING DATE: 25-JANUARY-1999  
ATTORNEY/AGENT INFORMATION:  
NAME: WIXON, HENRY N.  
REGISTRATION NUMBER: 32,073  
(C) ATTORNEY DOCKET NO. 104322.147CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-942-8400  
TELEFAX: 202-942-8484  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: Peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 35:  
US-09-828-870-35

Query Match 95.1%; Score 97; DB 11; Length 19;  
Best Local Similarity 100.0%; Pred. No. 6.7e-09;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MGQVGRQLAIGDDINRRY 20  
Db 1 MGQVGRQLAIGDDINRRY 19

RESULT 15  
US-10-189-294-4  
; Sequence 0, Application US/10189294  
; Publication No. US20030060615A1  
; GENERAL INFORMATION:  
; APPLICANT: Kiefer, Michael C.  
; Gibson, Helen L.  
; Fitzpatrick, Paul A.  
; Barr, Philip J.  
; TITLE OF INVENTION: A NOVEL BAK BINDING PROTEIN, DNA  
; ENCODING THE PROTEIN, AND METHODS OF USE THEREOF  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWN, THERESA A.  
; STREET: 1560 Broadway, Suite 1200  
; CITY: Denver  
; STATE: CO  
; COUNTRY: USA  
; ZIP: 80202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/189,294  
; FILING DATE: 01-Jul-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/381,488  
; FILING DATE: 11-Feb-2000  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWN, THERESA A.  
; REGISTRATION NUMBER: 32,547  
; REFERENCE/DOCKET NUMBER: 4147-15-PUS  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (303) 863-0223  
; TELEFAX: (303) 863-0223  
; INFORMATION FOR SEQ ID NO: /note= "Bak (delta)2 (delta)TM"  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 117 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: Protein  
; LOCATION: 1..117



SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-10-189-294-4

Query Match 95.1%; Score 97; DB 14; Length 117;  
Best Local Similarity 100.0%; Pred. No. 5e-08;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 MGQVGRQLAIIGDDINRRY 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1 MGQVGRQLAIIGDDINRRY 19

Search completed: January 25, 2005, 10:31:00  
Job time : 98.5 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 26, 2005, 00:02:31 ; Search time 38 Seconds  
(without alignments)  
34.904 Million cell updates/sec

Title: US-09-828-870-36

Perfect score: 102

Sequence: 1 TMGVGRQLAIGDDINRY 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A.COMB.pap:\*  
2: /cgn2\_6/ptodata/1/iaa/5B.COMB.pap:\*  
3: /cgn2\_6/ptodata/1/iaa/6A.COMB.pap:\*  
4: /cgn2\_6/ptodata/1/iaa/6B.COMB.pap:\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS.COMB.pap:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	102	100.0	20	3	US-09-236-385A-36
2	102	100.0	27	4	US-09-544-664B-4
3	102	100.0	28	1	US-08-440-391-2
4	102	100.0	28	1	US-08-440-391-18
5	102	100.0	28	2	US-08-908-597A-2
6	102	100.0	28	2	US-08-908-597A-18
7	102	100.0	28	3	US-09-236-385A-2
8	102	100.0	28	3	US-09-236-385A-18
9	102	100.0	28	5	PCT-US96-06122-2
10	102	100.0	28	5	PCT-US96-06122-18
11	102	100.0	36	1	US-08-440-391-14
12	102	100.0	36	2	US-08-908-597A-14
13	102	100.0	36	3	US-09-236-385A-14
14	102	100.0	36	5	PCT-US96-06122-14
15	102	100.0	152	1	US-08-471-058-22
16	102	100.0	210	3	US-08-471-058-22
17	102	100.0	210	4	US-08-471-057-22
18	102	100.0	211	1	US-08-321-071A-16
19	102	100.0	211	1	US-08-471-058-7
20	102	100.0	211	1	US-08-471-058-9
21	102	100.0	211	1	US-08-471-058-10
22	102	100.0	211	1	US-08-471-058-11
23	102	100.0	211	2	US-08-944-530-2
24	102	100.0	211	2	US-08-944-530-4
25	102	100.0	211	3	US-08-471-057-7
26	102	100.0	211	3	US-08-471-057-9
27	102	100.0	211	3	US-08-471-057-10

28	102	100.0	211	3	US-08-471-057-11	Sequence 11, Appl
29	102	100.0	211	4	US-09-381-488-2	Sequence 2, Appl
30	102	100.0	211	4	US-08-470-865-7	Sequence 7, Appl
31	102	100.0	211	4	US-08-470-865-9	Sequence 9, Appl
32	102	100.0	211	4	US-08-470-865-10	Sequence 10, Appl
33	102	100.0	211	4	US-08-470-865-11	Sequence 11, Appl
34	102	100.0	211	4	US-09-155-327G-13	Sequence 13, Appl
35	97	95.1	19	3	US-09-236-385A-35	Sequence 35, Appl
36	97	95.1	117	4	US-09-381-488-4	Sequence 23, Appl
37	97	95.1	141	1	US-08-471-058-23	Sequence 4, Appl
38	92	90.2	27	4	US-09-544-664B-5	Sequence 5, Appl
39	86	84.3	31	1	US-08-440-391-3	Sequence 3, Appl
40	86	84.3	31	1	US-08-440-391-16	Sequence 16, Appl
41	86	84.3	31	2	US-08-908-597A-3	Sequence 3, Appl
42	86	84.3	31	2	US-08-908-597A-16	Sequence 16, Appl
43	86	84.3	31	3	US-09-236-385A-3	Sequence 3, Appl
44	86	84.3	31	3	US-09-236-385A-16	Sequence 16, Appl
45	86	84.3	31	5	PCT-US96-06122-3	Sequence 3, Appl

#### ALIGNMENTS

##### RESULT 1

US-09-236-385A-36  
; Sequence 36, Application US/09236385A  
; Patent No. 6221615  
; GENERAL INFORMATION:  
; APPLICANT: CHITTENDEN, Thomas D.; and  
; LUTZ, Robert J.  
; TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH  
; MODULATE APOPTOSIS  
; NUMBER OF SEQUENCES: 41  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hale and Dorr  
; STREET: 1455 Pennsylvania Avenue, N.W.  
; CITY: Washington  
; STATE: D.C.  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/236.385A  
; FILING DATE: 25-Jan-1999  
; CLASSIFICATION: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WIXON, HENRY N.  
; REGISTRATION NUMBER: 32,073  
; TELECOMMUNICATION INFORMATION:  
; (C) ATTORNEY DOCKET NO. 104322.147CIP  
; TELEPHONE: 202-942-8400  
; TELEFAX: 202-942-8484  
; INFORMATION FOR SEQ ID NO: 36  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 36

Query Match 100.0%; Score 102; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 7.9e-11;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TMGVGRQLAIGDDINRY 20  
Db 1 TMGVGRQLAIGDDINRY 20

RESULT 2  
US-09-544-664B-4  
; Sequence 4, Application US/09544664B  
; Patent No. 6713280  
; GENERAL INFORMATION:  
; APPLICANT: Huang, Ziwei  
; APPLICANT: Wang, Jialun  
; APPLICANT: Zhang, Zhijia  
; APPLICANT: Shan, Simei  
; APPLICANT: Lu, Zhixian  
; TITLE OF INVENTION: Enhancement of Peptide Cellular Uptake  
; FILE REFERENCE: 8321-68  
; CURRENT APPLICATION NUMBER: US/09/544,664B  
; CURRENT FILING DATE: 2000-04-06  
; PRIOR APPLICATION NUMBER: PCT/US00/09352  
; PRIOR FILING DATE: 2000-04-06  
; PRIOR APPLICATION NUMBER: 60/128,202  
; PRIOR FILING DATE: 1999-04-07  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 27  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide  
; OTHER INFORMATION: segment from BH3 domain of a Bcl-2 superfamily  
; OTHER INFORMATION: polypeptide  
US-09-544-664B-4

Query Match 100.0%; Score 102; DB 4; Length 27;  
Best Local Similarity 100.0%; Pred. No. 1.1e-10;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TMGVGRLAIIGDDINRRY 20  
Db 4 TMGVGRLAIIGDDINRRY 23

RESULT 3  
US-08-440-391-2  
; Sequence 2, Application US/08440391  
; Patent No. 5656725  
; GENERAL INFORMATION:  
; APPLICANT: CHITTENDEN, Thomas D.; and  
; APPLICANT: LUTZ, Robert J.  
; TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH  
; TITLE OF INVENTION: MODULATE APOPTOSIS  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hale and Dorr  
; STREET: 1455 Pennsylvania Avenue, N.W.  
; CITY: Washington  
; STATE: D.C.  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/440,391  
; FILING DATE: 12-MAY-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WIXON, HENRY N.  
; REGISTRATION NUMBER: 32,073  
; REFERENCE/DOCKET NUMBER: 104322.147  
; TELEPHONE: 202-942-8400  
; TELEFAX: 202-942-8484  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:

; LENGTH: 28 amino acid  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-440-391-2  
Query Match 100.0%; Score 102; DB 1; Length 28;  
Best Local Similarity 100.0%; Pred. No. 1.2e-10;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TMGVGRLAIIGDDINRRY 20  
Db 4 TMGVGRLAIIGDDINRRY 23

RESULT 4  
US-08-440-391-18  
; Sequence 18, Application US/08440391  
; Patent No. 5656725  
; GENERAL INFORMATION:  
; APPLICANT: CHITTENDEN, Thomas D.; and  
; APPLICANT: LUTZ, Robert J.  
; TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH  
; TITLE OF INVENTION: MODULATE APOPTOSIS  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hale and Dorr  
; STREET: 1455 Pennsylvania Avenue, N.W.  
; CITY: Washington  
; STATE: D.C.  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/440,391  
; FILING DATE: 12-MAY-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WIXON, HENRY N.  
; REGISTRATION NUMBER: 32,073  
; REFERENCE/DOCKET NUMBER: 104322.147  
; TELEPHONE: 202-942-8400  
; TELEFAX: 202-942-8484  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 28 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-440-391-18

Query Match 100.0%; Score 102; DB 1; Length 28;  
Best Local Similarity 100.0%; Pred. No. 1.2e-10;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TMGVGRLAIIGDDINRRY 20  
Db 4 TMGVGRLAIIGDDINRRY 23

RESULT 5  
US-08-908-597A-2  
; Sequence 2, Application US/08908597A  
; Patent No. 5663795  
; GENERAL INFORMATION:  
; APPLICANT: CHITTENDEN, Thomas D.; and  
; APPLICANT: LUTZ, Robert J.  
; TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH  
; TITLE OF INVENTION: MODULATE APOPTOSIS

NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr  
STREET: 1455 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: D.C.  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/908,597A  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/440,391  
FILING DATE: 12-MAY-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: WIXON, HENRY N.  
REGISTRATION NUMBER: 32,073  
REFERENCE/DOCKET NUMBER: 104322.147  
TELEPHONE: 202-942-8400  
TELEFAX: 202-942-8484  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 28 amino acid  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-908-597A-2

Query Match 100.0%; Score 102; DB 2; Length 28;  
Best Local Similarity 100.0%; Pred. No. 1.2e-10;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TMGVGRLAIIGDDINRRY 20  
DB 4 TMGVGRLAIIGDDINRRY 23

## RESULT 6

US-08-908-597A-18  
Sequence 18, Application US/08908597A  
Patent No. 5863795  
GENERAL INFORMATION:  
APPLICANT: CHITTENDEN, Thomas D.; and  
ADDRESSEE: LUTZ, Robert J.  
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH  
MODULATE APOPTOSIS  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr  
STREET: 1455 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: D.C.  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/908,597A  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/440,391  
FILING DATE: 12-MAY-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: WIXON, HENRY N.

REGISTRATION NUMBER: 32,073  
REFERENCE/DOCKET NUMBER: 104322.147  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-942-8400  
TELEFAX: 202-942-8484  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 28 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-908-597A-18

Query Match 100.0%; Score 102; DB 2; Length 28;  
Best Local Similarity 100.0%; Pred. No. 1.2e-10;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TMGVGRLAIIGDDINRRY 20  
DB 4 TMGVGRLAIIGDDINRRY 23

## RESULT 7

US-09-236-385A-2  
Sequence 2, Application US/09236385A  
Patent No. 6221615  
GENERAL INFORMATION:  
APPLICANT: CHITTENDEN, Thomas D.; and  
ADDRESSEE: LUTZ, Robert J.  
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH  
MODULATE APOPTOSIS  
NUMBER OF SEQUENCES: 41  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr  
STREET: 1455 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: D.C.  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/236,385A  
FILING DATE: 25-Jan-1999  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: WIXON, HENRY N.  
REGISTRATION NUMBER: 32,073  
(C) ATTORNEY DOCKET NO. 104322.147CIP

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-942-8400  
TELEFAX: 202-942-8484

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 28 amino acid

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-236-385A-2

Query Match 100.0%; Score 102; DB 3; Length 28;  
Best Local Similarity 100.0%; Pred. No. 1.2e-10;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TMGVGRLAIIGDDINRRY 20  
DB 4 TMGVGRLAIIGDDINRRY 23

## RESULT 8

US-09-236-385A-18  
; Sequence 18, Application US/09236385A  
; Patent No. 6221615  
; GENERAL INFORMATION:  
; APPLICANT: CHITTENDEN, Thomas D.; and  
; LUTZ, Robert J.  
; TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH  
; MODULATE APOPTOSIS  
; NUMBER OF SEQUENCES: 41  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hale and Dorr  
; STREET: 1455 Pennsylvania Avenue, N.W.  
; CITY: Washington  
; STATE: D.C.  
; ZIP: 20004  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA: US/09/236,385A  
; FILING DATE: 25-Jan-1999  
; CLASSIFICATION: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WIXON, HENRY N.  
; REGISTRATION NUMBER: 32,073  
; TELECOMMUNICATION INFORMATION: (C) ATTORNEY DOCKET NO. 104322.147CIP  
; TELEPHONE: 202-942-8400  
; TELEFAX: 202-942-8484  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 28 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:  
US-09-236-385A-18  
  
Query Match 100.0%; Score 102; DB 3; Length 28;  
Best Local Similarity 100.0%; Pred. No. 1.2e-10;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 TMGQVGRQLAIIIGDDINRRY 20  
Db 4 TMGQVGRQLAIIIGDDINRRY 23  
  
RESULT 9  
PCT-US96-06122-2  
; Sequence 2, Application PC/TUS9606122  
; GENERAL INFORMATION:  
; APPLICANT: IMMUNOGEN, INC.  
; TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS  
; WHICH MODULATE APOPTOSIS  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hale and Dorr  
; STREET: 1455 Pennsylvania Avenue, N.W.  
; CITY: Washington  
; STATE: D.C.  
; ZIP: 20004  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/06122  
; FILING DATE: HERewith  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; Sequence 2, Application PC/TUS9606122  
; GENERAL INFORMATION:  
; APPLICANT: IMMUNOGEN, INC.  
; TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS  
; WHICH MODULATE APOPTOSIS  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hale and Dorr  
; STREET: 1455 Pennsylvania Avenue, N.W.  
; CITY: Washington  
; STATE: D.C.  
; ZIP: 20004  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/06122  
; FILING DATE: HERewith  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/440,391  
; FILING DATE: 12-MAY-1995  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WIXON, HENRY N.  
; REGISTRATION NUMBER: 32,073  
; REFERENCE/DOCKET NUMBER: 104322.147PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-942-8400  
; TELEFAX: 202-942-8484  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 28 amino acid  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; PCT-US96-06122-2  
  
Query Match 100.0%; Score 102; DB 5; Length 28;  
Best Local Similarity 100.0%; Pred. No. 1.2e-10;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 TMGQVGRQLAIIIGDDINRRY 20  
Db 4 TMGQVGRQLAIIIGDDINRRY 23  
  
RESULT 10  
PCT-US96-06122-18  
; Sequence 18, Application PC/TUS9606122  
; GENERAL INFORMATION:  
; APPLICANT: IMMUNOGEN, INC.  
; TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS  
; WHICH MODULATE APOPTOSIS  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hale and Dorr  
; STREET: 1455 Pennsylvania Avenue, N.W.  
; CITY: Washington  
; STATE: D.C.  
; ZIP: 20004  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/06122  
; FILING DATE: HERewith  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; Sequence 18, Application PC/TUS9606122  
; GENERAL INFORMATION:  
; APPLICANT: IMMUNOGEN, INC.  
; TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS  
; WHICH MODULATE APOPTOSIS  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hale and Dorr  
; STREET: 1455 Pennsylvania Avenue, N.W.  
; CITY: Washington  
; STATE: D.C.  
; ZIP: 20004  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/06122  
; FILING DATE: HERewith  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; Sequence 18, Application PC/TUS9606122  
; GENERAL INFORMATION:  
; APPLICANT: IMMUNOGEN, INC.  
; TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS  
; WHICH MODULATE APOPTOSIS  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hale and Dorr  
; STREET: 1455 Pennsylvania Avenue, N.W.  
; CITY: Washington  
; STATE: D.C.  
; ZIP: 20004  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/06122  
; FILING DATE: HERewith  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; Sequence 18, Application PC/TUS9606122  
; GENERAL INFORMATION:  
; APPLICANT: IMMUNOGEN, INC.  
; TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS  
; WHICH MODULATE APOPTOSIS  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hale and Dorr  
; STREET: 1455 Pennsylvania Avenue, N.W.  
; CITY: Washington  
; STATE: D.C.  
; ZIP: 20004  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/06122  
; FILING DATE: HERewith  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:

Query Match 100.0%; Score 102; DB 5; Length 28;  
Best Local Similarity 100.0%; Pred. No. 1.2e-10;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TMGQVGRQLAIIGDDINRRY 20  
Db 4 TMGQVGRQLAIIGDDINRRY 23

RESULT 11  
US-08-440-391-14  
; Sequence 14, Application US/08440391  
; Patent No. 5656725  
; GENERAL INFORMATION:  
; APPLICANT: CHITTENDEN, Thomas D.; and  
; APPLICANT: LUTZ, Robert J.  
; TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH  
; TITLE OF INVENTION: MODULATE APOPTOSIS  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hale and Dorr  
; STREET: 1455 Pennsylvania Avenue, N.W.  
; CITY: Washington  
; STATE: D.C.  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/440,391  
; FILING DATE: 12-MAY-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WIXON, HENRY N.  
; REGISTRATION NUMBER: 32,073  
; REFERENCE/DOCKET NUMBER: 104322.147  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-942-8400  
; TELEFAX: 202-942-8484  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 36 base pairs  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-440-391-14

Query Match 100.0%; Score 102; DB 1; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1.5e-10;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TMGQVGRQLAIIGDDINRRY 20  
Db 6 TMGQVGRQLAIIGDDINRRY 25

RESULT 12  
US-08-908-597A-14  
; Sequence 14, Application US/08908597A  
; Patent No. 5863795  
; GENERAL INFORMATION:  
; APPLICANT: CHITTENDEN, Thomas D.; and  
; APPLICANT: LUTZ, Robert J.  
; TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH  
; TITLE OF INVENTION: MODULATE APOPTOSIS  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hale and Dorr  
; STREET: 1455 Pennsylvania Avenue, N.W.  
; CITY: Washington  
; STATE: D.C.  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/908,597A  
; FILING DATE:  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/440,391  
; FILING DATE: 12-MAY-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WIXON, HENRY N.  
; REGISTRATION NUMBER: 32,073  
; REFERENCE/DOCKET NUMBER: 104322.147  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-942-8400  
; TELEFAX: 202-942-8484  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 36  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-908-597A-14

Query Match 100.0%; Score 102; DB 2; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1.5e-10;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TMGQVGRQLAIIGDDINRRY 20  
Db 6 TMGQVGRQLAIIGDDINRRY 25

RESULT 13  
US-09-236-385A-14  
; Sequence 14, Application US/09236385A  
; Patent No. 6221615  
; GENERAL INFORMATION:  
; APPLICANT: CHITTENDEN, Thomas D.; and  
; APPLICANT: LUTZ, Robert J.  
; TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH  
; MODULATE APOPTOSIS  
; NUMBER OF SEQUENCES: 41  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hale and Dorr  
; STREET: 1455 Pennsylvania Avenue, N.W.  
; CITY: Washington  
; STATE: D.C.  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/236,385A  
; FILING DATE: 25-Jan-1999  
; CLASSIFICATION: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WIXON, HENRY N.  
; REGISTRATION NUMBER: 32,073  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-942-8400  
; TELEFAX: 202-942-8484  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 36 base pairs  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:  
US-09-236-385A-14

APPLICANT: BARR, PHILIP J.  
TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA  
SEQUENCES, AND METHODS OF USE THEREOF  
TITLE OF INVENTION: ENCODING THE PROTEINS AND METHODS OF USE THEREOF  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/471,057  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/320,157



Query Match 100.0%; Score 102; DB 4; Length 210;  
Best Local Similarity 100.0%; Pred. No. 1.2e-09;

```

RESULT 19
US-08-471-058-7
; Sequence 7, Application US/08471058
; Patent No. 5770443
; GENERAL INFORMATION:
; APPLICANT: Kiefer, Michael C.
; APPLICANT: Barr, Philip J.
; TITLE OF INVENTION: NOVEL APOPTOSIS
; TITLE OF INVENTION: PROTEINS, DI
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 24

```

```
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: MORRISON & FOERSTER
;; STREET: 755 PAGE MILL ROAD
;; CITY: Palo Alto
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 94304-1018
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSeq for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/471,058
;; FILING DATE: 06-JUN-1995
;; CLASSIFICATION: 800
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/320,157
;; FILING DATE: 07-OCT-1994
;; APPLICATION NUMBER: 08/160,067
;; FILING DATE: 30-NOV-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Lehnhardt, Susan K
;; REGISTRATION NUMBER: 33,943
;; REFERENCE/DOCKET NUMBER: 23647-20007.12
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-813-5600
;; TELEFAX: 415-494-0792
;; TELEX: 706141
;; INFORMATION FOR SEQ ID NO: 7:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 211 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; FRAGMENT TYPE: internal
;; US-08-471-058-7

Query Match          100.0%; Score 102; DB 1; Length 211;
Best Local Similarity 100.0%; Pred. No. 1.2e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TMGVGRLAIIGDDINRRY 20
Db      70 TMGVGRLAIIGDDINRRY 89

RESULT 20
US-08-471-058-9
; Sequence 9, Application US/08471058
; Patent No. 5770443
; GENERAL INFORMATION:
; APPLICANT: Kiefer, Michael C.
; APPLICANT: Barr, Philip J.
; TITLE OF INVENTION: NOVEL APOPTOSIS MODULATING
; TITLE OF INVENTION: PROTEINS, DNA ENCODING THE PROTEINS AND METHODS OF USE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,058
```

```
;; FILING DATE: 06-JUN-1995
;; CLASSIFICATION: 800
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/320,157
;; FILING DATE: 07-OCT-1994
;; APPLICATION NUMBER: 08/160,067
;; FILING DATE: 30-NOV-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Lehnhardt, Susan K
;; REGISTRATION NUMBER: 33,943
;; REFERENCE/DOCKET NUMBER: 23647-20007.12
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-813-5600
;; TELEFAX: 415-494-0792
;; TELEX: 706141
;; INFORMATION FOR SEQ ID NO: 9:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 211 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; FRAGMENT TYPE: internal
;; US-08-471-058-9

Query Match          100.0%; Score 102; DB 1; Length 211;
Best Local Similarity 100.0%; Pred. No. 1.2e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TMGVGRLAIIGDDINRRY 20
Db      70 TMGVGRLAIIGDDINRRY 89

RESULT 21
US-08-471-058-10
; Sequence 10, Application US/08471058
; Patent No. 5770443
; GENERAL INFORMATION:
; APPLICANT: Kiefer, Michael C.
; APPLICANT: Barr, Philip J.
; TITLE OF INVENTION: NOVEL APOPTOSIS MODULATING
; TITLE OF INVENTION: PROTEINS, DNA ENCODING THE PROTEINS AND METHODS OF USE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,058
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/320,157
; FILING DATE: 07-OCT-1994
; APPLICATION NUMBER: 08/160,067
; FILING DATE: 30-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Lehnhardt, Susan K
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20007.12
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-813-5600
; TELEFAX: 415-494-0792
```

```
;
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 211 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-471-058-10

Query Match 100.0%; Score 102; DB 1; Length 211;
Best Local Similarity 100.0%; Pred. No. 1.2e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TMGVGRLAIIGDDINRRY 20
Db 70 TMGVGRLAIIGDDINRRY 89

RESULT 22
US-08-471-058-11
; Sequence 11, Application US/08471058
; Patent No. 5770443
; GENERAL INFORMATION:
; APPLICANT: Kiefer, Michael C.
; APPLICANT: Barr, Philip J.
; TITLE OF INVENTION: NOVEL APOPTOSIS MODULATING
; TITLE OF INVENTION: PROTEINS, DNA ENCODING THE PROTEINS AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ FOR WINDOWS VERSION 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,058
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/320,157
; FILING DATE: 07-OCT-1994
; APPLICATION NUMBER: 08/160,067
; FILING DATE: 30-NOV-1993
; NAME: LEHNHARDT, SUSAN K.
; ATTORNEY/AGENT INFORMATION:
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20007.12
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-813-5600
; TELEFAX: 415-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 211 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-471-058-11

Query Match 100.0%; Score 102; DB 1; Length 211;
Best Local Similarity 100.0%; Pred. No. 1.2e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TMGVGRLAIIGDDINRRY 20
Db 70 TMGVGRLAIIGDDINRRY 89

RESULT 23
US-08-944-530-2
; Sequence 2, Application US/08944530
; Patent No. 5998131
; GENERAL INFORMATION:
; APPLICANT: BARR, PHILIP J.
; APPLICANT: KIEFER, MICHAEL C.
; TITLE OF INVENTION: METHODS OF SCREENING FOR THERAPEUTIC
; TITLE OF INVENTION: AGENTS USING NOVEL APOPTOSIS-MODULATING PROTEINS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/944,530
; FILING DATE: 07-OCT-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/426,529
; FILING DATE: 20-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: LEHNHARDT, SUSAN K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20007.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 211 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-944-530-2

Query Match 100.0%; Score 102; DB 2; Length 211;
Best Local Similarity 100.0%; Pred. No. 1.2e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TMGVGRLAIIGDDINRRY 20
Db 70 TMGVGRLAIIGDDINRRY 89

RESULT 24
US-08-944-530-4
; Sequence 4, Application US/08944530
; Patent No. 5998131
; GENERAL INFORMATION:
; APPLICANT: BARR, PHILIP J.
; APPLICANT: KIEFER, MICHAEL C.
; TITLE OF INVENTION: METHODS OF SCREENING FOR THERAPEUTIC
; TITLE OF INVENTION: AGENTS USING NOVEL APOPTOSIS-MODULATING PROTEINS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304-1018
```

## RESULT 27

```
US-08-471-057-10
; Sequence 10, Application US/08471057
; Patent No. 6015687
; GENERAL INFORMATION:
; APPLICANT: KIEFER, MICHAEL C.
; APPLICANT: BARR, PHILIP J.
; TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
; TITLE OF INVENTION: ENCODING THE PROTEINS AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471.057
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/320,157
; FILING DATE: 07-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: LEHNHARDT, SUSAN K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20007.20
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 211 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-471-057-10

Query Match 100.0%; Score 102; DB 3; Length 211;
Best Local Similarity 100.0%; Pred. No. 1.2e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TMQGVGRQLAIGDDINRRY 20
| | | | | | | | | | | | | | | | | | | | |
Db 70 TMQGVGRQLAIGDDINRRY 89

RESULT 28
US-08-471-057-11
; Sequence 11, Application US/08471057
; Patent No. 6015687
; GENERAL INFORMATION:
; APPLICANT: KIEFER, MICHAEL C.
; APPLICANT: BARR, PHILIP J.
; TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
; TITLE OF INVENTION: ENCODING THE PROTEINS AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/381,488
; FILING DATE: 11-Feb-2000
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWN, THERESA A.
; REGISTRATION NUMBER: 32,547
; REFERENCE/DOCKET NUMBER: 4147-15-PUS
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 211 amino acids
; TYPE: amino acid
; COMPUTER: IBM PC compatible
```

```
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471.057
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/320,157
; FILING DATE: 07-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: LEHNHARDT, SUSAN K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20007.20
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 211 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-471-057-11

Query Match 100.0%; Score 102; DB 3; Length 211;
Best Local Similarity 100.0%; Pred. No. 1.2e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TMQGVGRQLAIGDDINRRY 20
| | | | | | | | | | | | | | | | | | | | |
Db 70 TMQGVGRQLAIGDDINRRY 89

RESULT 29
US-09-381-488-2
; Sequence 2, Application US/09381488
; Patent No. 6441135
; GENERAL INFORMATION:
; APPLICANT: Kiefer, Michael C.
; Fitzpatrick, Helen L.
; Fitzpatrick, Paul A.
; Barz, Philip J.
; TITLE OF INVENTION: A NOVEL Bak BINDING PROTEIN, DNA
; ENCODING THE PROTEIN, AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWN, THERESA A.
; STREET: 1560 Broadway, Suite 1200
; CITY: Denver
; STATE: CO
; COUNTRY: USA
; ZIP: 80202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/381,488
; FILING DATE: 11-Feb-2000
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWN, THERESA A.
; REGISTRATION NUMBER: 32,547
; REFERENCE/DOCKET NUMBER: 4147-15-PUS
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 211 amino acids
; TYPE: amino acid
```

```

;
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
; US-09-381-488-2
;
;
; Query Match 100.0%; Score 102; DB 4; Length 211;
; Best Local Similarity 100.0%; Pred. No. 1.2e-09;
; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 TMGQVGRQLAIIIGDDINRRY 20
; | | | | | | | | | | | | | | | | | | | |
; DB 70 TMGQVGRQLAIIIGDDINRRY 89
;
;
; RESULT 30
; US-08-470-865-7
; Sequence 7, Application US/08470865
; Patent No. 6586395
; GENERAL INFORMATION:
; APPLICANT: KIEFER, MICHAEL C.
; APPLICANT: BARR, PHILIP J.
; TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
; TITLE OF INVENTION: ENCODING THE PROTEINS AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470.865
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/320.157
; FILING DATE: 07-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: LEHNHARDT, SUSAN K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20007.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 211 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-470-865-9
;
; Query Match 100.0%; Score 102; DB 4; Length 211;
; Best Local Similarity 100.0%; Pred. No. 1.2e-09;
; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 TMGQVGRQLAIIIGDDINRRY 20
; | | | | | | | | | | | | | | | | | | | |
; DB 70 TMGQVGRQLAIIIGDDINRRY 89
;
;
; RESULT 32
; US-08-470-865-10
; Sequence 10, Application US/08470865
; Patent No. 6586395
; GENERAL INFORMATION:
; APPLICANT: KIEFER, MICHAEL C.
; APPLICANT: BARR, PHILIP J.
; TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
; TITLE OF INVENTION: ENCODING THE PROTEINS AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470.865
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/320.157
; FILING DATE: 07-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: LEHNHARDT, SUSAN K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20007.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 211 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-470-865-7
;
; Query Match 100.0%; Score 102; DB 4; Length 211;
; Best Local Similarity 100.0%; Pred. No. 1.2e-09;
; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 TMGQVGRQLAIIIGDDINRRY 20
; | | | | | | | | | | | | | | | | | | | |
; DB 70 TMGQVGRQLAIIIGDDINRRY 89
;
;
; RESULT 31
; US-08-470-865-9
; Sequence 9, Application US/08470865
; Patent No. 6586395
; GENERAL INFORMATION:

```

```
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/320,157
; FILING DATE: 07-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: LEHNHARDT, SUSAN K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20007.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 211 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-470-865-10
;
Query Match 100.0%; Score 102; DB 4; Length 211;
Best Local Similarity 100.0%; Pred. No. 1.2e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TMGQVGRQLAIIIGDDINRRY 20
Db 70 TMGQVGRQLAIIIGDDINRRY 89

RESULT 33
US-08-470-865-11
; Sequence 11, Application US/08470865
; Patent No. 6586395
; GENERAL INFORMATION:
; APPLICANT: KIEFER, MICHAEL C.
; APPLICANT: BARR, PHILIP J.
; TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
; TITLE OF INVENTION: ENCODING THE PROTEINS AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,865
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/320,157
; FILING DATE: 07-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: LEHNHARDT, SUSAN K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20007.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 211 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-470-865-11
; Sequence 11, Application US/09155327G
; Patent No. 6790637
; GENERAL INFORMATION:
; APPLICANT: AMRAD Operations Pty Ltd
; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-2, BELONGS TO THE bcl-2
; TITLE OF INVENTION: FAMILY OF APOPTOSIS-CONTROLLING GENES
; FILE REFERENCE: 2096584
; CURRENT APPLICATION NUMBER: US/09/155,327G
; CURRENT FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: P88965
; PRIOR FILING DATE: 1996-03-27
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 13
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-09-155-327G-13
;
Query Match 100.0%; Score 102; DB 4; Length 211;
Best Local Similarity 100.0%; Pred. No. 1.2e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TMGQVGRQLAIIIGDDINRRY 20
Db 70 TMGQVGRQLAIIIGDDINRRY 89

Search completed: January 26, 2005, 00:52:16
Job time : 39 secs
```

**This Page Blank (uspto)**



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 25, 2005, 10:06:02 ; Search time 24.5 Seconds  
(without alignments)  
78.544 Million cell updates/sec

Title: US-09-828-870-36  
Perfect score: 102  
Sequence: 1 TMQVGRQLAIGDDINRRY 20

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	102	100.0	211	2 S58873	Bak protein - huma
2	102	100.0	211	2 S58875	cdn-2 protein - hu
3	48	47.1	1329	2 T33136	hypothetical prote
4	46.5	45.6	357	2 T06308	protein phosphatas
5	46	45.1	244	2 G82418	transcription regu
6	46	45.1	747	2 C75545	phosphoribosylform
7	46	45.1	833	2 AE0564	ht/K <sub>+</sub> -exchanging A
8	46	45.1	834	1 C64779	probable copper-tr
9	46	45.1	834	2 E85546	probable ATPase yb
10	46	45.1	834	2 A90696	Cu(II)-translocatio
11	46	45.1	915	2 H82104	cation transport A
12	46	45.1	1226	2 S44824	P54P2.1 protein -
13	45.5	44.6	532	2 JN0084	phytoene dehydroge
14	45	44.1	426	2 S58884	phosphopyruvate hy
15	45	44.1	426	2 H71967	enolase - Helicoba
16	44.5	43.6	774	2 JC7265	neprilysin (EC 3.4
17	44	43.1	234	2 AC3205	IS66 family Orf4 (
18	44	43.1	258	2 H75027	ey v-atpase proteo
19	44	43.1	261	2 E71213	probable chemorece
20	44	43.1	465	2 T48374	UDPG glucosyltrans
21	44	43.1	521	2 T34482	hypothetical prote
22	44	43.1	593	2 S75352	ABC-type transport
23	44	43.1	693	2 G82618	pilus biogenesis p
24	44	43.1	803	1 E70041	probable copper-tr
25	43.5	42.6	355	2 H84643	probable protein p
26	43	42.2	65	2 G75258	conserved hypothet
27	43	42.2	248	2 T44822	hypothetical prote
28	43	42.2	356	2 S71460	ribose-phosphate d
29	43	42.2	356	2 A53433	ribose-phosphate d

30	43	42.2	400	2 T33073	hypothetical prote
31	43	42.2	424	2 F84165	hypothetical prote
32	43	42.2	424	2 T08229	probable transposa
33	43	42.2	424	2 T08249	probable transposa
34	43	42.2	444	2 JQ1185	phosphopyruvate hy
35	43	42.2	446	2 T03267	probable phosphopy
36	43	42.2	446	2 T02221	probable enolase (
37	43	42.2	447	2 G86940	hypothetical prote
38	43	42.2	475	2 T48031	probable allantoad
39	43	42.2	498	2 T37527	hypothetical prote
40	43	42.2	664	2 D96633	hypothetical prote
41	43	42.2	770	2 T23999	hypothetical prote
42	43	42.2	827	2 B95969	Probable H <sub>2</sub> /K <sub>+</sub> -exc
43	43	42.2	380	2 T51053	hypothetical prote
44	42	41.2	826	2 D95330	cu2+-exporting ATP
45	41.5	40.7	300	2 H83384	probable epoxide h

## ALIGNMENTS

## RESULT 1

S58873  
Bak protein - human  
N;Alternate names: bcl-2 homolog; cdn-1 protein  
C;Species: Homo sapiens (man)  
C;Date: 15-Feb-1996 #sequence revision 01-Mar-1996 #text\_change 09-Jul-2004  
C;Accession: S58873; S58872; S58874  
R;Chittenden, T.; Harrington, E.A.; O'Connor, R.; Flemington, C.; Lutz, R.J.; Evan, G.I.  
Nature 374, 733-736, 1995  
A;Title: Induction of apoptosis by the Bcl-2 homologue Bak.  
A;Reference number: S58873; MUID:95231653; PMID:7715730  
A;Accession: S58873  
A;Status: preliminary; nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-211 <CHI>  
A;Cross-references: EMBL:X84213; EMBL:U23765; NID:g758797; PIDN:AAA93066.1; PID:g758  
R;Farrow, S.N.; White, J.H.M.; Martinou, I.; Raven, T.; Pun, K.T.; Grinham, C.J.; Marti.  
Nature 374, 731-733, 1995  
A;Title: Cloning of a bcl-2 homologue by interaction with adenovirus E1B 19K.  
A;Reference number: S58872; MUID:95231652; PMID:7715729  
A;Accession: S58872  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-211 <FAR>  
A;Cross-references: EMBL:X84213; NID:g804984; PIDN:CAA58997.1; PID:g804985  
R;Kiefer, M.C.; Brauer, M.J.; Powers, V.C.; Wu, J.J.; Umansky, S.R.; Tomei, L.D.; Barr.  
Nature 374, 736-739, 1995  
A;Title: Modulation of apoptosis by the widely distributed Bcl-2 homologue Bak.  
A;Reference number: S58874; MUID:95231654; PMID:7715731  
A;Accession: S58874  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-211 <KIE>  
A;Cross-references: EMBL:U16811; NID:g595923; PIDN:AAA74466.1; PID:g595924  
C;Genetics:  
A;Gene: GDB:BAK  
A;Cross-references: GDB:635887

Query Match 100.0%; Score 102; DB 2; Length 211;  
Best Local Similarity 100.0%; Pred. No. 4.3e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TMQVGRQLAIGDDINRRY 20  
|||||  
Db 70 TMQVGRQLAIGDDINRRY 89

## RESULT 2

S58875  
cdn-2 protein - human  
C;Species: Homo sapiens (man)  
C;Date: 15-Feb-1996 #sequence\_revision 01-Mar-1996 #text\_change 09-Jul-2004

C;Accession: S58875  
R;Kiefer, M.C.; Brauer, M.J.; Powers, V.C.; Wu, J.J.; Umansky, S.R.; Tomei, L.D.; Barr,  
Nature 374, 736-739, 1995  
A;Title: Modulation of apoptosis by the widely distributed Bcl-2 homologue Bak.  
A;Reference number: S58874; MUID:95231654; PMID:7715731  
A;Accession: S58875  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-211 <KIE>  
A;Cross-references: UNIPROT:Q13014; EMBL:U16812; NID:G595925; PIDN:AAA74467.1; PID:G59595  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1994

Query Match 100.0%; Score 102; DB 2; Length 211;  
Best Local Similarity 100.0%; Pred. No. 4.3e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TMGQVGRQLAIIIGDDINRRY 20  
Db 70 TMGQVGRQLAIIIGDDINRRY 89

RESULT 3  
T33136  
hypothetical protein C45G7.6 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T33136  
R;Dante, M.; Wamsley, P.  
submitted to the EMBL Data Library, May 1998  
A;Description: The sequence of C. elegans cosmid C45G7.  
A;Reference number: Z21288  
A;Accession: T33136  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-1329 <DAN>  
A;Cross-references: UNIPROT:O76356; EMBL:AF067611; PIDN:AAC19184.1; GSPDB:GN00022; CESP:  
A;Experimental source: strain Bristol N2; clone C45G7  
C;Genetics:  
A;Gene: CESP:C45G7.6  
A;Map position: 4  
A;Introns: 27/3; 70/3; 110/3; 356/1; 544/2; 649/3; 750/2; 846/3; 1021/3; 1064/3; 1247/3

Query Match 47.1%; Score 48; DB 2; Length 1329;  
Best Local Similarity 50.0%; Pred. No. 23;  
Matches 10; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 TMGQVGRQLAIIIGDDINRRY 20  
Db 526 TIQGVDSLKIIGNGNRKF 545

RESULT 4  
T06308  
protein phosphatase 2C homolog Fl1C18.60 - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 30-Apr-1999 #sequence\_revision 30-Apr-1999 #text\_change 09-Jul-2004  
C;Accession: T06308  
R;Revan, M.; Terry, N.; Ardiles, W.; Buysshaert, C.; Dasseville, R.; De Clerck, R.; De  
wees, H.W.; Mayer, K.F.X.; Schueller, C.  
submitted to the Protein Sequence Database, April 1999  
A;Reference number: Z15589  
A;Accession: T06308  
A;Molecule type: DNA  
A;Residues: 1-357 <BEV>  
A;Cross-references: UNIPROT:Q9SZ53; EMBL:AL049607; GSPDB:GN00062; ATSP:Fl1C18.60  
A;Experimental source: cultivar Columbia; BAC clone Fl1C18  
C;Genetics:  
A;Gene: ATSP:Fl1C18.60  
A;Map position: 4  
A;Introns: 39/3; 61/1; 97/2; 148/3; 190/3; 232/1; 257/3; 275/2; 293/3  
C;Superfamily: human phosphoprotein phosphatase 1A

Query Match 45.6%; Score 46.5; DB 2; Length 357;

Best Local Similarity 58.8%; Pred. No. 9.3;  
Matches 10; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

QY 3 GQVG-RQLAIIIGDDINR 18  
Db 104 GQGWRELAVLGDINK 120

RESULT 5  
G82418  
transcription regulator Tetr family VCA0767 [imported] - Vibrio cholerae (strain N16961)  
C;Species: Vibrio cholerae  
C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004  
C;Accession: G82418  
R;Heidelber, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;  
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I.;  
R. R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
Nature 406, 477-483, 2000  
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.  
A;Reference number: A82035; MUID:20406833; PMID:10952301  
A;Accession: G82418  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-244 <HEI>  
A;Cross-references: UNIPROT:Q9KLH7; GB:AE004405; GB:AE003853; NID:G9658186; PIDN:AAF966  
A;Experimental source: serogroup O1; strain N16961; biotype El Tor  
C;Genetics:  
A;Gene: VCA0767  
A;Map position: 2

Query Match 45.1%; Score 46; DB 2; Length 244;  
Best Local Similarity 40.0%; Pred. No. 7.3;  
Matches 8; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 TMGQVGRQLAIIIGDDINRRY 20  
Db 134 TSGEIERLVESLADDYNRQY 153

RESULT 6  
C75545  
phosphoribosylformylglycinamide synthase II - Deinococcus radiodurans (strain R1)  
C;Species: Deinococcus radiodurans  
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C;Accession: C75545  
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;  
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.;  
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.  
Science 286, 1571-1577, 1999  
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.  
A;Reference number: A75250; MUID:20036896; PMID:10567266  
A;Accession: C75545  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-747 <WHI>  
A;Cross-references: UNIPROT:Q9RXT4; GB:AE001884; GB:AE000513; NID:G6457890; PIDN:AAF098  
A;Experimental source: strain R1  
C;Genetics:  
A;Gene: DR0222  
A;Map position: 1  
C;Superfamily: phosphoribosylformylglycinamide synthase component II

Query Match 45.1%; Score 46; DB 2; Length 747;  
Best Local Similarity 44.4%; Pred. No. 25;  
Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 TMGQVGRQLAIIIGDDINR 18  
Db 195 TMGEVGNQIVYVGSKTGR 212

RESULT 7  
AE0564

H+/K+-exchanging ATPase (EC 3.6.3.10) - Salmonella enterica subsp. enterica serovar Typh  
 C;Species: Salmonella enterica subsp. enterica serovar Typhi  
 A;Note: this species has also been called Salmonella typhi  
 C;Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
 C;Accession: AE0564  
 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Main, J.; Churcher,  
 th, T.; Connerton, P.; Cronin, P.; Davies, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,  
 S.; Moulle, S.; O'Gaora, P.  
 Nature 413, 848-852, 2001  
 A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;  
 A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov  
 A;Reference number: AB0502; MUID:21534947; PMID:11677608  
 A;Accession: AE0564  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-833 <PAR>  
 A;Cross-references: GB:AL513382; PIDN:CAD04983.1; PID:gl16501768; GSPDB:GNO0176  
 C;Genetics:  
 A;Gene: STY0544  
 C;Superfamily: Bacillus probable copper-transporting ATPase yvqX; ATPase nucleotide-bind  
 C;Keywords: hydrolase

Query Match 45.1%; Score 46; DB 2; Length 833;  
 Best Local Similarity 66.7%; Pred. No. 29;  
 Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GRQLAIIIGDDIN 17  
 |||:|:|:|  
 Db 711 GRQVAMVGDGIN 722

RESULT 8  
 C64779  
 Probable copper-transporting ATPase (EC 3.6.1.-) - Escherichia coli (strain K-12)  
 C;Species: Escherichia coli  
 C;Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 09-Jul-2004  
 C;Accession: C64779  
 R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co  
 A.; Rose, D.J.; Mau, B.; Shao, Y.  
 Science 277, 1453-1462, 1997  
 A;Title: The complete genome sequence of Escherichia coli K-12.  
 A;Reference number: A64720; MUID:97426617; PMID:9278503  
 A;Accession: C64779  
 A;Status: nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-834 <BLAT>  
 A;Cross-references: UNIPROT:Q59385; GB:AE000154; GB:U00096; NID:gl1786683; PIDN:AAC73586.  
 A;Experimental source: strain K-12, substrain MG1655  
 C;Genetics:  
 A;Gene: ybaR  
 C;Superfamily: Bacillus probable copper-transporting ATPase yvqX; ATPase nucleotide-bind  
 C;Keywords: ATP; copper binding; hydrolase; ion transport; metal binding; phosphoprotein  
 F;9-38/Domain: heavy-metal-associated homology <HMA1>  
 F;105-134/Domain: heavy-metal-associated homology <HMA2>  
 F;189-205/Domain: transmembrane #status predicted <TM1>  
 F;218-234/Domain: transmembrane #status predicted <TM2>  
 F;224-568/Domain: ATPase transduction domain homology <ATT>  
 F;438-454/Domain: transmembrane #status predicted <TM3>  
 F;468-484/Domain: transmembrane #status predicted <TM4>  
 F;631-647/Domain: transmembrane #status predicted <TM5>  
 F;643-785/Domain: ATPase nucleotide-binding domain homology <ATN>  
 F;806-822/Domain: transmembrane #status predicted <TM6>  
 F;108-110.113/Binding site: copper (Met, Cys, Cys) #status predicted  
 F;523/Active site: Asp (aspartylphosphate intermediate) #status predicted

Query Match 45.1%; Score 46; DB 1; Length 834;  
 Best Local Similarity 66.7%; Pred. No. 29;  
 Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GRQLAIIIGDDIN 17  
 |||:|:|:|  
 Db 712 GRQVAMVGDGIN 723

RESULT 9  
 E85546  
 Probable ATPase ybaR [imported] - Escherichia coli (strain O157:H7, substrain EDL933)  
 C;Species: Escherichia coli  
 C;Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004  
 C;Accession: E85546  
 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhe  
 iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca  
 Nature 409, 529-533, 2001  
 A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
 A;Reference number: A85480; MUID:21074935; PMID:11206551  
 A;Accession: E85546  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-834 <STO>  
 A;Cross-references: UNIPROT:Q8XD24; GB:AE005174; NID:gl2513357; PIDN:AGS4833.1; GSPDB:  
 A;Experimental source: strain O157:H7, substrain EDL933  
 C;Genetics:  
 A;Gene: ybaR  
 C;Superfamily: Bacillus probable copper-transporting ATPase yvqX; ATPase nucleotide-bin

Query Match 45.1%; Score 46; DB 2; Length 834;  
 Best Local Similarity 66.7%; Pred. No. 29;  
 Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GRQLAIIIGDDIN 17  
 |||:|:|:|  
 Db 712 GRQVAMVGDGIN 723

RESULT 10  
 A90696  
 CuI]-translocation P-type ATPase [imported] - Escherichia coli (strain O157:H7, substr  
 C;Species: Escherichia coli  
 C;Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 09-Jul-2004  
 C;Accession: A90696  
 R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Iehii, K.; Yokoyama, K.; Han, C.G  
 G.; Yaguchi, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
 DNA Res. 8, 11-22, 2001  
 A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen  
 A;Reference number: A99629; MUID:21156231; PMID:11258796  
 A;Accession: A90696  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-834 <HAY>  
 A;Cross-references: UNIPROT:Q8XD24; GB:BA000007; PIDN:BA833960.1; PID:gl33559994; GSPDB:  
 A;Experimental source: strain O157:H7, substrain RMD 0509952  
 C;Genetics:  
 A;Gene: ECG0537  
 C;Superfamily: Bacillus probable copper-transporting ATPase yvqX; ATPase nucleotide-bin

Query Match 45.1%; Score 46; DB 2; Length 834;  
 Best Local Similarity 66.7%; Pred. No. 29;  
 Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GRQLAIIIGDDIN 17  
 |||:|:|:|  
 Db 712 GRQVAMVGDGIN 723

RESULT 11  
 H82104  
 cation transport ATPase, EI-E2 family VC2215 [imported] - Vibrio cholerae (strain N1696  
 C;Species: Vibrio cholerae  
 C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004  
 C;Accession: H82104  
 R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.  
 chardson, D.; Ermlaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers,  
 l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
 Nature 406, 477-483, 2000  
 A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.  
 A;Reference number: A82035; MUID:20406833; PMID:10952301

A;Accession: H82104  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-915 <HEI>  
A;Cross-references: UNIPROT:Q9KPT7; GB:AE004293; GB:AE003852; NID:g9656766; PIDN:AAF9535  
A;Experimental source: serogroup O1; strain N16961; biotype E1 Tor  
C;Genetics:  
A;Gene: VC2215  
A;Map position: 1  
C;Superfamily: Bacillus probable copper-transporting ATPase yvqX; ATPase nucleotide-bind

Query Match 45.1%; Score 46; DB 2; Length 915;  
Best Local Similarity 64.3%; Pred. No. 32;  
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 QVGRQLAIIGDDIN 17  
Db 786 QQGRKVAMIGDGIN 799  
|||:|||||

RESULT 12  
S44824  
F54F2.1 protein - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 14-Sep-1994 #sequence\_revision 12-May-1995 #text\_change 09-Jul-2004  
A;Accession: S44824  
R;Anderson, K.  
submitted to the EMBL Data Library, September 1993  
A;Description: Sequence of the C. elegans cosmid F54F2.  
A;Reference number: S44817  
A;Accession: S44824  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-1226 <AND>  
A;Cross-references: UNIPROT:P34446; EMBL:L23645; NID:g388603; PID:g388605  
C;Genetics:  
A;Introns: 58/2; 137/3; 179/1; 316/2; 393/1; 551/3; 597/2; 662/2; 899/3; 1178/3  
C;Keywords: cytoskeleton; transmembrane protein

Query Match 45.1%; Score 46; DB 2; Length 1226;  
Best Local Similarity 53.8%; Pred. No. 44;  
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 QVGRQLAIIGDD 15  
Db 359 GVFGKQIAVGGDD 371  
|||:|||||

RESULT 13  
JN0084  
phytoene dehydrogenase (EC 1.3.-.-) - Aphanocapsa sp. (PCC 6714)  
N;Alternate names: phytoene desaturase  
C;Species: Aphanocapsa sp.  
C;Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 09-Jul-2004  
C;Accession: JN0084  
R;Schmidt, A.; Sandmann, G.  
Gene 91, 113-117, 1990  
A;Title: Cloning and nucleotide sequence of the crtI gene encoding phytoene dehydrogenase  
A;Reference number: JN0084; MUID:90382685; PMID:2119326  
A;Accession: JN0084  
A;Molecule type: DNA  
A;Residues: 1-532 <SCH>  
A;Cross-references: UNIPROT:P21134; GB:M55647; GB:M33237; NID:g141989; PIDN:AAA62573.1;  
A;Note: the authors translated the codon CAG for residue 380 as Gly  
C;Comment: This enzyme catalyzes the symmetrical introduction of two double bonds at C-1  
C;Genetics:  
A;Gene: crtI  
C;Superfamily: Aphanocapsa phytoene dehydrogenase  
C;Keywords: carotenoid biosynthesis; membrane bound; oxidoreductase

Query Match 44.6%; Score 45.5; DB 2; Length 532;  
Best Local Similarity 42.9%; Pred. No. 21;  
Matches 9; Conservative 7; Mismatches 2; Indels 3; Gaps 1;

QY 2 MGQVGRQLAI---IGDINRR 19  
Db 140 IQGTRRLQLLEFICEDVHRQ 160  
|||:|||||

RESULT 14  
S58684  
phosphopyruvate hydratase (EC 4.2.1.11) - Helicobacter pylori (strains 26695 and others)  
N;Alternate names: enolase  
C;Species: Helicobacter pylori  
C;Date: 29-Nov-1995 #sequence\_revision 17-Sep-1997 #text\_change 09-Jul-2004  
A;Accession: B64539; S58684  
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.  
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenn  
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Matthey, L  
Nature 388, 539-547, 1997  
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C  
A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.  
A;Reference number: A64520; MUID:97394467; PMID:9252185  
A;Accession: B64539  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-426 <TOM>  
A;Cross-references: UNIPROT:P48285; GB:AE000536; GB:AE000511; NID:g2313230; PIDN:AAD072  
A;Experimental source: strain 26695  
R;Schmitt, W.; Odenbreit, S.; Heuermann, D.; Haas, R.  
Mol. Gen. Genet. 248, 563-572, 1995  
A;Title: Cloning of the Helicobacter pylori recA gene and functional characterization o  
A;Reference number: S58683; MUID:96027928; PMID:7476856  
A;Accession: S58684  
A;Molecule type: DNA  
A;Residues: 1-25, '1', 27-68 <SCH>  
A;Cross-references: EMBL:Z35478  
C;Genetics:  
A;Gene: HP0154  
C;Function:  
A;Description: catalyzes the reversible dehydration of 2-phospho-D-glyceric acid to pho  
A;Pathway: glycolysis  
C;Superfamily: enolase  
C;Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase; magnesium  
F;42/Binding site: magnesium 2 (Ser) #status predicted  
F;205,338/Active site: Glu, Lys #status predicted  
F;242,286,313/Binding site: magnesium 1 (Asp, Glu, Asp) #status predicted

Query Match 44.1%; Score 45; DB 2; Length 426;  
Best Local Similarity 46.2%; Pred. No. 20;  
Matches 6; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 4 QVGRQLAIIGDDI 16  
Db 303 ELGRQIQLVGGDL 315  
|||:|||||

RESULT 15  
H71967  
enolase - Helicobacter pylori (strain J99)  
C;Species: Helicobacter pylori  
A;Variety: strain J99  
C;Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 09-Jul-2004  
C;Accession: H71967  
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.  
Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;  
Nature 397, 176-180, 1999  
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric pat  
A;Reference number: A71800; MUID:99120557; PMID:9923682  
A;Accession: H71967  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-426 <ARN>  
A;Cross-references: UNIPROT:Q9ZMS6; GB:AE001453; GB:AE001439; NID:g4154651; PIDN:AAD0572  
A;Experimental source: strain J99  
C;Genetics:



**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 25, 2005, 10:06:01 ; Search time 132 Seconds  
(without alignments)  
87.178 Million cell updates/sec

Title: US-09-828-870-36

Perfect score: 102  
Sequence: 1 TMQVGRQLAIGDDINRRY 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt 02:\*\*

1: uniprot\_sprot:\*\*

2: uniprot\_trembl:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	102	100.0	80	2	077738	O77738 sus scrofa
2	102	100.0	190	2	Q8NFF3	Q8NFF3 homo sapien
3	102	100.0	211	1	BAK2_HUMAN	Q13014 homo sapien
4	102	100.0	211	1	BAK_HUMAN	Q16611 homo sapien
5	102	100.0	211	2	CAG33700	Cag33700 homo sapi
6	101	99.0	163	2	Q9M2S6	Q9m2s6 ovis aries
7	92	90.2	151	2	Q91WX5	Q91wx5 mus musculu
8	92	90.2	151	2	AAH57589	Aah57589 mus muscu
9	92	90.2	208	1	BAK_MOUSE	Q08734 mus musculu
10	92	90.2	209	2	Q8C364	Q8c284 mus musculu
11	92	90.2	209	2	Q9JK59	Q9jks9 rattus norv
12	50	49.0	264	2	Q74116	Q74116 lactobacill
13	50	49.0	264	2	AAR27400	Aar27400 lactobaci
14	50	49.0	264	2	AAS09524	Aas09524 lactobaci
15	49	48.0	336	1	K6P3_BACTN	Q8a289 bacteroides
16	48	47.1	395	2	Q72B37	Q72b37 desulfovibr
17	48	47.1	395	2	AAS96278	Aas96278 desulfovi
18	48	47.1	1329	2	Q76356	Q76356 caenorhabdi
19	47	46.1	265	2	Q89Q04	Q89q04 bradyrhizob
20	47	46.1	373	2	Q6HA04	Q6ha04 pagothenia
21	47	46.1	1430	2	Q8PLI2	Q8pl12 xanthomonas
22	46.5	45.6	357	2	Q8S2S3	Q8s2s3 arabidopsis
23	46	45.1	244	2	Q9KHL7	Q9klh7 vibrio chol
24	46	45.1	375	2	Q6HA05	Q6ha05 pagothenia
25	46	45.1	454	2	Q8H716	Q8h716 phytophthor
26	46	45.1	593	2	Q7VBJ6	Q7vbj6 prochloroc
27	46	45.1	747	1	PURL_DEIRA	Q9xt44 deinococcus
28	46	45.1	832	1	ATCU_SALTI	Q8z884 salmonella
29	46	45.1	832	1	ATCU_SALTY	Q8zr95 salmonella
30	46	45.1	833	1	ATCU_ECO57	Q8xd24 escherichia
31	46	45.1	833	1	ATCU_ECOLI	Q59385 escherichia

32 46 45.1 834 2 Q7C2W2 Q7c2w2 shigella fl  
33 46 45.1 834 2 Q83SE2 Q83se2 shigella fl  
34 46 45.1 834 2 Q8FK77 Q8fk77 escherichia  
35 46 45.1 915 1 ATCU\_VIBCH Q9kz77 vibrio chol  
36 46 45.1 1226 1 PAT2\_CAEEL P34446 caenorhabdi  
37 45.5 44.6 426 2 Q6DA85 Q6da85 erwinia car  
38 45.5 44.6 532 1 CRTI\_SYNY4 P21134 synechocyst  
39 45 44.1 195 2 Q9WX82 Q9wx82 paracoccus  
40 45 44.1 211 2 Q89BY1 Q89by1 bradyrhizob  
41 45 44.1 297 1 PYRB\_HELHP Q7vlt3 helicobacte  
42 45 44.1 351 2 Q9L8Q2 Q9l8q2 pseudomonas  
43 45 44.1 371 2 Q8VWE2 Q8vwe2 streptomyce  
44 45 44.1 419 2 Q8AB89 Q8ab89 bacteroides  
45 45 44.1 426 1 ENO\_HELPJ Q9zms6 helicobacte

#### ALIGNMENTS

##### RESULT 1

O77738 PRELIMINARY; PRT; 80 AA.  
AC O77738;  
DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Bak protein (Fragment).  
GN NamesBak;  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Darmer D.;  
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ001204; CAA04598.1;  
DR GO; GO:0042981; P:regulation of apoptosis; IEA.  
DR InterPro; IPR000712; Bcl2\_BH.  
DR InterPro; IPR002475; BCL2\_FAMILY.  
DR SMART; SM00337; BCL; 1.  
DR PROSITE; PS00662; BCL2\_FAMILY; 1.  
DR PROSITE; PS01259; BH3; 1.  
FT NON\_TER 1  
FT NON\_TER 80  
SQ SEQUENCE 80 AA; 8818 MW; FDLAF83BD7D59C86 CRC64;

Query Match 100.0%; Score 102; DB 2; Length 80;  
Best Local Similarity 100.0%; Pred. No. 5.2e-08;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TMQVGRQLAIGDDINRRY 20

|||||  
21 TMQVGRQLAIGDDINRRY 40

##### RESULT 2

Q8NFF3 PRELIMINARY; PRT; 190 AA.  
AC Q8NFF3;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Pro-apoptotic protein BAKM variant.  
GN Name=BAK;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
Ma J.;

Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.

RL EMBL; AF520590; AAM74949.1; -  
DR HSP; Q16611; 1BXL.  
DR GO; GO:0042581; P:regulation of apoptosis; IEA.  
DR InterPro; IPR000712; BCL2 BH.  
DR InterPro; IPR002475; BCL2 family.  
DR Pfam; PF00452; Bcl-2; 1.  
DR SMART; SM00337; BCL; 1.  
DR PROSITE; PS0062; BCL2\_FAMILY; 1.  
DR PROSITE; PS01080; BH1; 1.  
DR PROSITE; PS01258; BH2; 1.  
DR PROSITE; PS01259; BH3; 1.  
SQ SEQUENCE 190 AA; 21231 MW; A9D4EB8526D0897B CRC64;

Query Match 100.0%; Score 102; DB 2; Length 190;  
Best Local Similarity 100.0%; Pred. No. 1.2e-07;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TMGQVGRQLAIIGDDINRRY 20  
|||||  
Db 49 TMGQVGRQLAIIGDDINRRY 68  
|||||

RESULT 3

BAK2 HUMAN STANDARD; PRT; 211 AA.  
AC Q13014;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Putative Bcl-2 homologous antagonist/killer 2 (Apoptosis regulator BAK-2).  
GN Name=BCL2L7P1; Synonyms=BAK2;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95231654; PubMed=7715731;  
RA Kiefer M.C., Brauer M.J., Powers V.C., Wu J.J., Umansky S.R., Tomei L.D., Barr P.J.;  
RT "Modulation of apoptosis by the widely distributed Bcl-2 homologue Bak.";  
RT Nature 374:736-739 (1995).  
RL Nature 374:736-739 (1995).  
CC -I- FUNCTION: In the presence of an appropriate stimulus, accelerates programmed cell death by binding to, and antagonizing the a repressor Bcl-2 or its adenovirus homolog E1B 19k protein.  
CC -I- SUBUNIT: Forms heterodimers with Bcl-2, E1B 19k protein, and Bcl-2 X(L).  
CC -I- SUBCELLULAR LOCATION: Membrane-associated (Potential).  
CC -I- TISSUE SPECIFICITY: Expressed in a wide variety of tissues, with highest levels in the heart and skeletal muscle.  
CC -I- DOMAIN: Interact BH3 domain is required by BIK, BID, BAK, BAD and BAX for their pro-apoptotic activity and for their interaction with anti-apoptotic members of the Bcl-2 family. Apoptotic members of the Bcl-2 family.  
CC -I- SIMILARITY: Belongs to the Bcl-2 family.  
CC -I- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.  
CC -I- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.  
CC -I- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.  
CC -I- CAUTION: This is probably the product of a pseudogene.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
DR EMBL; U16812; AAA74467.1; -  
DR FIR; S58875; S58875.

DR HSP; Q16611; 1BXL.  
DR Genew; HGNC:996; BCL2L7P1.  
DR GO; GO:0016020; C:membrane; NAS.  
DR GO; GO:0006917; P:induction of apoptosis; NAS.  
DR InterPro; IPR000712; BCL2 BH.  
DR InterPro; IPR002475; BCL2 family.  
DR Pfam; PF00452; Bcl-2; 1.  
DR SMART; SM00337; BCL; 1.  
DR PROSITE; PS0062; BCL2\_FAMILY; 1.  
DR PROSITE; PS01080; BH1; 1.  
DR PROSITE; PS01258; BH2; 1.  
DR PROSITE; PS01259; BH3; 1.  
KW Apoptosis; Hypothetical protein; Transmembrane.  
FT DOMAIN 74 88 BH3.  
FT DOMAIN 117 136 BH1.  
FT DOMAIN 169 184 BH2.  
FT TRANSMEM 188 205 Potential.  
SQ SEQUENCE 211 AA; 23411 MW; 703875EC4DCC1D3 CRC64;

Query Match 100.0%; Score 102; DB 1; Length 211;  
Best Local Similarity 100.0%; Pred. No. 1.4e-07;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TMGQVGRQLAIIGDDINRRY 20  
|||||  
Db 70 TMGQVGRQLAIIGDDINRRY 89  
|||||

RESULT 4

BAK HUMAN STANDARD; PRT; 211 AA.  
AC Q16611; Q92533;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 01-OCT-2004 (Rel. 45, Last annotation update)  
DE Bcl-2 homologous antagonist/killer (Apoptosis regulator BAK) (BCL2-like 7 protein).  
GN Name=BAK1; Synonyms=BAK, BCL2L7;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=B-cell.  
RX MEDLINE=95231652; PubMed=7715729;  
RA Farrow S.N., White J.H.M., Martinou J., Raven T., Pun K.-T., Grinham C.J., Martinou J.C., Brown R.;  
RT "Cloning of a bcl-2 homologue by interaction with adenovirus E1B 19K.";  
RT Nature 374:731-733 (1995).  
RL Nature 374:731-733 (1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95231653; PubMed=7715730;  
RA Chittenden T., Harrington E.A., O'Connor R., Flemington C., Lutz R.J., Evan G.I., Guild B.C.;  
RA "Induction of apoptosis by the Bcl-2 homologue Bak.";  
RT "Induction of apoptosis by the Bcl-2 homologue Bak.";  
RL Nature 374:733-736 (1995).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95231654; PubMed=7715731;  
RA Kiefer M.C., Brauer M.J., Powers V.C., Wu J.J., Umansky S.R., Tomei L.D., Barr P.J.;  
RT "Modulation of apoptosis by the widely distributed Bcl-2 homologue Bak.";  
RL Nature 374:736-739 (1995).  
RN [4]  
RP SEQUENCE FROM N.A. AND VARIANTS VAL-28 AND ARG-69.  
RA Rieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W., Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;  
RT "NIHNS-SNPs, environmental genome project, NIHNS ES15478, Department of Genome Sciences, Seattle, WA (URL: <http://egp.gs.washington.edu>).";



Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.

[5]  
 Sequence from N.A.  
 MEDLINE=22935763; PubMed=14574404; DOI=10.1038/nature02055;  
 Mungall A.J., Palmer S.A., Sims S.K., Edwards C.A., Ashurst J.L.,  
 Wilming L., Jones M.C., Horton R., Hunt S.E., Scott C.E.,  
 Gilbert J.G.R., Clamp M.E., Bethel G., Milne S., Ainscough R.,  
 Almeida J.P., Ambrose K.D., Andrews T.D., Ashwell R.I.S.,  
 Babbage A.K., Baggeley C.L., Bailey J., Banerjee R., Barker D.J.,  
 Barlow K.P., Bates K., Beare D.M., Beasley H., Beasley O., Bird C.P.,  
 Blakey S.E., Bray-Allen S., Brook J., Brown A.J., Brown J.Y.,  
 Burford D.C., Burkill W., Burton J., Carter C., Carter N.P.,  
 Chapman J.C., Clark S.Y., Clark S., Cleve C.M., Clegg S., Cobley V.,  
 Collier R.E., Collins J.E., Colman L.K., Corby N.R., Coville G.J.,  
 Culley K.M., Dhali P., Davies J., Dunn M., Earthrowl M.E.,  
 Ellington A.B., Evans K.A., Faulkner L., Francis M.D., Frankish A.,  
 Frankland J., French L., Garner P., Garnett J., Ghori M.J.,  
 Gilby L.M., Gillson C.J., Glithero R.J., Grafham D.V., Grant M.,  
 Gribble S., Griffiths C., Griffiths M.N.D., Hall R., Halls K.S.,  
 Hammond S., Harley J.L., Hart E.A., Heath P.D., Heathcote R.,  
 Holmes S.J., Howden P.J., Howe K.L., Howell G.R., Huckle E.,  
 Humphray S.J., Humphries M.D., Hunt A.R., Johnson C.M., Joy A.A.,  
 Kay M., Keenan S.J., Kimberley A.M., King A., Laird G.K., Langford C.,  
 Lawlor S., Leongamornlert D.A., Leversha M., Lloyd C.R., Lloyd D.M.,  
 Loveland J.E., Lovell J., Martin S., Mashreghi-Mohammadi M.,  
 Maen G.L., Matthews L., McCann O.T., McLaren S.J., McIlroy K.,  
 McMurray A., Moore M.J.F., Mullikin J.C., Niblett D., Nickerson T.,  
 Novik K.L., Oliver K., Overton-Larty E.K., Parker A., Patel R.,  
 Pearce A.V., Peck A.I., Phillimore B.J.C.T., Phillips S., Plumb R.W.,  
 Porter K.M., Ramsey Y., Ranby S.A., Rice C.M., Ross M.T., Seale S.M.,  
 Shera H.K., Sheridan E., Skuce C.D., Smith S., Smith M., Spraggon L.,  
 Squares S.L., Steward C.A., Sycamore N., Tamlyn-Hall G., Tester J.,  
 Theaker A.J., Thomas D.W., Thorpe A., Tracey A., Tromans A., Tubby B.,  
 Wall M., Wallis J.M., West A.P., White S.S., Whitehead S.L., Wray P.W.,  
 Whittaker H., Wild A., Willey D.J., Wilmer T.E., Wood J.M., Wyatt J.C.,  
 Wyatt J.C., Young L., Younger R.M., Bentley D.R., Coulson A.,  
 Durbin R., Hubbard T., Sulston J.E., Dunham I., Rogers J., Beck S.;  
 "The DNA sequence and analysis of human chromosome 6";  
 Nature 425:805-811(2003).  
 [6]  
 Sequence from N.A.  
 TISSUE=Lung;  
 MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,  
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
 Raha S.S., Loquellano N.A., Peters G.J., Abranson R.D., Mullaby S.J.,  
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 Vialla D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 Blakeley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 Butterfield F.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
 Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences";  
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 [7]  
 Sequence of 96-206 FROM N.A.  
 Eguchi H., Hayashi S.;  
 "Estrogen alters expression of apoptosis-regulators, Bcl-2, Bcl-xL and  
 Bak, as well as susceptibility to therapeutic agents of human breast  
 cancer cells";  
 Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.  
 [8]  
 MUTAGENESIS, AND FUNCTION OF BH3 DOMAIN.  
 MEDLINE=96091131; PubMed=8521816;  
 Chittenden T., Flemington C., Houghton A.B., Ebb R.G., Gallo G.J.,  
 Elangovan B., Chinnadurai G., Lutz R.J.;  
 "A conserved domain in Bak, distinct from BH1 and BH2, mediates cell  
 death and protein binding functions.";  
 EMBO J. 14:5589-5596(1995).  
 [9]  
 STRUCTURE BY NMR OF 72-87.  
 MEDLINE=97172562; PubMed=9020082;  
 Sattler M., Liang H., Nettesheim D., Meadows R.P., Harlan J.E.,  
 Eberstadt M., Yoon H.S., Shuker S.B., Chang B.S., Minn A.J.,  
 Thompson C.B., Feak S.W.;  
 "Structure of Bcl-xL-Bak peptide complex: recognition between  
 regulators of apoptosis";  
 Science 275:983-986(1997).  
 CC -i- FUNCTION: In the presence of an appropriate stimulus, accelerates  
 programmed cell death by binding to, and antagonizing the a  
 repressor Bcl-2 or its adenovirus homolog E1B 19K protein.  
 CC -i- SUBUNIT: Forms heterodimers with Bcl-2, E1B 19K protein, and Bcl-  
 x(L).  
 CC -i- SUBCELLULAR LOCATION: Membrane-bound (potential).  
 CC -i- TISSUE SPECIFICITY: Expressed in a wide variety of tissues, with  
 highest levels in the heart and skeletal muscle.  
 CC -i- DOMAIN: Inactive BH3 domain is required by BIK, BID, BAK, BAD and  
 BAX for their pro-apoptotic activity and for their interaction  
 with anti-apoptotic members of the Bcl-2 family.  
 CC -i- SIMILARITY: Belongs to the Bcl-2 family.  
 CC -i- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.  
 CC -i- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.  
 CC -i- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use by non-profit institutions as long as its content is in no way  
 modified and this statement is not removed. Usage by and for commercial  
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 -----  
 ENBL; X84213; CAA58997.1; --  
 ENBL; U23765; AAA93066.1; --  
 ENBL; U16811; AAA74466.1; --  
 ENBL; AY260471; AAO74828.1; --  
 ENBL; Z93017; CAB65626.1; --  
 ENBL; BC004431; AAH04431.1; --  
 ENBL; D88397; BAA13606.1; --  
 ENBL; D88396; BAA13606.1; JOINED.  
 PIR; S58873; S58873.  
 PDB; 1BXL; NMR; B=72-87.  
 Genew; HGNC:949; BAK1.  
 MIM; 600516; --  
 GO; GO:0008637; P.apoptotic mitochondrial changes; TAS.  
 DR InterPro; IPR000712; Bcl2\_BH.  
 DR InterPro; IPR002475; BCL2 family.  
 DR Pfam; PF00452; Bcl-2; 1.  
 DR PROSITE; PS01080; BCL2 FAMILY; 1.  
 DR PROSITE; PS01080; BH1; 1.  
 DR PROSITE; PS01258; BH2; 1.  
 DR PROSITE; PS01259; BH3; 1.  
 DR 3D-structure; Apoptosis; Polymorphism; Transmembrane.  
 FT DOMAIN 74 88  
 FT DOMAIN 117 136 BH3.  
 FT DOMAIN 169 184 BH2.  
 FT TRANSMEM 188 205 Potential.  
 FT VARIANT 28 28 A -> V.  
 FT VARIANT 69 69 /FTID=VAR\_018829.  
 FT TURN 74 75 S -> R.  
 FT HELIX 76 84 /FTID=VAR\_018830.  
 FT TURN 85 85  
 SQ SEQUENCE 211 AA; 23409 MW; A2200FE72A46D04E CRC64;  
 Query Match 100.0%; Score 102; DB 1; Length 211;

Best Local Similarity 100.0%; Pred. No. 1.4e-07;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TMGQVGRQLAIGDDINRRY 20  
|||||  
DB 70 TMGQVGRQLAIGDDINRRY 89

RESULT 5  
CAG33700 PRELIMINARY; PRT; 211 AA.  
AC CAG33700;  
DT 01-JUN-2004 (TrEMBLrel. 27, Created)  
DT 01-JUN-2004 (TrEMBLrel. 27, Last sequence update)  
DT 01-JUN-2004 (TrEMBLrel. 27, Last annotation update)  
DE BAK1 protein.  
GN BAK1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;  
RT "Cloning of human full open reading frames in Gateway(TM) system entry  
RT vector (pDONR201)";  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; CR457419; CAG33700.1; -;  
SQ SEQUENCE 211 AA; 23409 MW; A2200FE72A46D04E CRC64;

Query Match 100.0%; Score 102; DB 2; Length 211;  
Best Local Similarity 100.0%; Pred. No. 1.4e-07;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TMGQVGRQLAIGDDINRRY 20  
|||||  
DB 70 TMGQVGRQLAIGDDINRRY 89

RESULT 6  
Q9MZS6 PRELIMINARY; PRT; 163 AA.  
AC Q9MZS6;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Bak protein (Fragment).  
OS Ovis aries (Sheep).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Caprinae; Ovis.  
OX NCBI\_TaxID=9940;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Murray J.F., Dong Y.B., Leigh A.J., Scaramuzzi R.J., Carter N.D.;  
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF164518; AAR9533.1; -;  
DR GO; GO:0042981; P:regulation of apoptosis; IEA.  
DR InterPro; IPR000712; BCL2 BH.  
DR InterPro; IPR002475; BCL2\_family.  
DR Pfam; PF00452; Bcl-2; 1.  
DR SMART; SM00337; BCL1; 1.  
DR PROSITE; PS00682; BCL2\_FAMILY; 1.  
DR PROSITE; PS01080; BH1; 1.  
DR PROSITE; PS01258; BH2; 1.  
DR PROSITE; PS01259; BH3; 1.  
FT NON\_TER 1  
FT TER 163  
SQ SEQUENCE 163 AA; 18039 MW; FB35E8A8C53AD5B CRC64;

Query Match 99.0%; Score 101; DB 2; Length 163;  
Best Local Similarity 95.0%; Pred. No. 1.5e-07;

Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TMGQVGRQLAIGDDINRRY 20  
|||||  
DB 29 TMGQVGRQLAIGDDINRRY 48

RESULT 7  
Q91WX5 PRELIMINARY; PRT; 151 AA.  
AC Q91WX5;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE N-BAK1.  
GN Name=Bak1;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NMRI; TISSUE=Neuronal;  
RX MEDLINE=21238300; PubMed=11278671;  
RA Sun Y.F., Yu L.Y., Saarma M., Timmusk T., Arumae U.;  
RT "Neuron-specific Bcl-2 homology 3 domain-only splice variant of Bak is  
RT anti-apoptotic in neurons, but pro-apoptotic in non-neuronal cells.";  
RL J. Biol. Chem. 276:16240-16247 (2001).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6; TISSUE=Brain;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Schaefer C.F., Bhat N.K.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahing J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6; TISSUE=Brain;  
RA Strausberg R.;  
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF402617; AAL01876.1; -;  
DR EMBL; BC057589; AAB57589.1; -;  
DR HSSP; Q16611; 1BXL.  
DR MGD; MGI:1097161; Bak1.  
DR GO; GO:0008635; P:caspace activation via cytochrome c; IMP.  
DR InterPro; IPR00712; BCL2 BH.  
DR InterPro; IPR002475; BCL2\_family.  
DR Pfam; PF0452; Bcl-2; 1.  
DR PROSITE; PS00682; BCL2\_FAMILY; 1.  
DR PROSITE; PS01259; BH3; 1.  
SQ SEQUENCE 151 AA; 16402 MW; 18C13BFF86E4F33B CRC64;

Query Match 90.2%; Score 92; DB 2; Length 151;  
Best Local Similarity 89.5%; Pred. No. 3.6e-06;  
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

QY 2 MGQVGRQLAIGDDINRRY 20
DB 69 LGQVGRQLAIGDDINRRY 87

RESULT 8
AAH57589
ID AAH57589 PRELIMINARY; PRT; 151 AA.
AC AAH57589;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Bcl-2 protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX Strausberg R.;
RA Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC057589; AAH57589.1; -.
SQ SEQUENCE 151 AA; 16402 MW; 18C13BFF86B4F33B CRC64;

Query Match 90.2%; Score 92; DB 2; Length 151;
Best Local Similarity 89.5%; Pred. No. 3.6e-06;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 MGQVGRQLAIGDDINRRY 20
DB 69 LGQVGRQLAIGDDINRRY 87

RESULT 9
BAK_MOUSE
ID BAK_MOUSE STANDARD; PRT; 208 AA.
AC O08734;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE Bcl-2 homologous antagonist/killer (Apoptosis regulator BAK).
GN Name=Bak1; Synonyms=Bak;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=Swiss; TISSUE=Liver;
RX MEDLINE=97446138; PubMed=9299236;
RA Ulrich E., Kauffmann-Zeh A., Hueber A.O., Williamson J.,
RA Chittenden T., Ma A., Evan G.I.;
RT "Gene structure, cDNA sequence, and expression of murine Bak, a
RL proapoptotic Bcl-2 family member.";
RL Genomics 44:195-200 (1997).
CC -1- FUNCTION: In the presence of an appropriate stimulus, accelerates
CC programmed cell death by binding to, and antagonizing the a
CC repressor Bcl-2 or its adenovirus homolog E1B 19k protein (By
CC similarity).
CC -1- SUBUNIT: Forms heterodimers with Bcl-2, E1B 19k protein, and Bcl-
CC X (L) (By similarity).
CC -1- SUBCELLULAR LOCATION: Membrane-associated (Potential).
CC -1- TISSUE SPECIFICITY: Widely expressed.
CC -1- DOMAIN: Intact BH3 domain is required by BIK, BID, BAK, BAD and
CC BAX for their pro-apoptotic activity and for their interaction
CC with anti-apoptotic members of the Bcl-2 family (By similarity).
CC -1- SIMILARITY: Belongs to the Bcl-2 family.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC EMBL; Y13231; CAA73684.1; -.
CC HSPSP; Q16611; 1BX1.
CC GMD; GGI:1097161; Bak1.
CC GO; GO:0008635; P: caspase activation via cytochrome c; IMP.
CC InterPro; IPR000712; BCL2_BH.
CC InterPro; IPR002475; BCL2_family.
CC Pfam; PF00452; Bcl-2; 1_Pfam.
CC PROSITE; PS50062; BCL2_FAMILY; 1.
CC PROSITE; PS01080; BH1; 1.
CC PROSITE; PS01258; BH2; 1.
CC PROSITE; PS01259; BH3; 1.
CC KW Apoptosis; Transmembrane.
CC FT DOMAIN 71 85 BH3.
CC FT DOMAIN 114 133 BH1.
CC FT DOMAIN 166 181 BH2.
CC FT TRANSMEM 185 202 Potential.
CC SQ SEQUENCE 208 AA; 23300 MW; DAFCL1B160C523C9 CRC64;

Query Match 90.2%; Score 92; DB 1; Length 208;
Best Local Similarity 89.5%; Pred. No. 4.9e-06;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 MGQVGRQLAIGDDINRRY 20
DB 68 LGQVGRQLAIGDDINRRY 86

RESULT 10
Q8C264
ID Q8C264 PRELIMINARY; PRT; 209 AA.
AC Q8C264;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus NOD-derived CD11c +ve dendritic cells cDNA, RIKEN full-
DE length enriched library, clone.F63004J23 product:BCL2-
DE antagonist/killer 1, full insert sequence.
GN Name=Bak1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

```

```

RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=NOD;
RX  MEDLINE=99279253; PubMed=10349636;
RA  Carninci P., Hayashizaki Y.;
RT  "High-efficiency full-length cDNA cloning.";
RL  Meth. Enzymol. 303:19-44 (1999).
RN  [2]
RP  SEQUENCE FROM N.A.
RC  STRAIN=NOD;
RX  MEDLINE=21085660; PubMed=11217851;
RA  RIKEN FANTOM Consortium;
RT  "Functional annotation of a full-length mouse cDNA collection.";
RL  Nature 409:685-690 (2001).
RN  [3]
RP  SEQUENCE FROM N.A.
RC  STRAIN=NOD;
RA  The FANTOM Consortium,
RT  "Analysis of the mouse transcriptome based on functional annotation of
RT  60,770 full-length cDNAs.";
RL  Nature 420:563-573 (2002).
RN  [4]
RP  SEQUENCE FROM N.A.
RC  STRAIN=NOD;
RX  MEDLINE=20499374; PubMed=11042159;
RA  Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA  Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT  "Normalization and subtraction of cap-trapper-selected cDNAs to
RT  prepare full-length cDNA libraries for rapid discovery of new genes.";
RL  Genome Res. 10:1617-1630 (2000).
RN  [5]
RP  SEQUENCE FROM N.A.
RC  STRAIN=NOD;
RX  MEDLINE=20530913; PubMed=11076861;
RA  Shibata K., Itoh M., Aizawa K., Katsunai T., Tashiro H., Itoh M.,
RA  Konno H., Akiyama J., Nishi K., Kitesunai T., Nishine T., Harada A.,
RA  Sumi N., Ishii Y., Nakamura S., Hazama M., Ikegami T., Kashiwagi K.,
RA  Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA  Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
RA  Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsumura S., Kawai J.,
RA  Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT  "RIKEN integrated sequence analysis (RISA) system-384-format
RT  sequencing pipeline with 384 multicapillary sequencer.";
RL  Genome Res. 10:1757-1771 (2000).
RN  [6]
RP  SEQUENCE FROM N.A.
RC  STRAIN=NOD;
RA  Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA  Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA  Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA  Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA  Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA  Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA  Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA  Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA  Saeki D., Shibata K., Shinagawa A., Shiraki T., Soabe Y., Tagami M.,
RA  Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA  Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL  Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AK089220; BAC40796.1; -.
DR  HSP; Q16611; 1BLX.
DR  MGD; MGI:1097161; Baki.
DR  GO; GO:0008635; P:caspace activation via cytochrome c; IMP.
DR  InterPro; IPR000712; BCL2_EH.
DR  InterPro; IPR002475; BCL2_family.
DR  Pfam; PF00452; Bcl-2; 1.
DR  SMART; SM00337; BCL; 1.
DR  PROSITE; PS00662; BCL2_FAMILY; 1.
DR  PROSITE; PS01258; BH2; 1.
DR  PROSITE; PS01259; BH3; 1.
SQ  SEQUENCE 209 AA; 23234 MW; 55E72D29A8AAFD18 CRC64;

```

```

Query Match      90.2%; Score 92; DB 2; Length 209;
Best Local Similarity 89.5%; Pred. No. 4.9e-06;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY  2 MGQVGRQLAIIIGDDINRRY 20
   :|||||:|||||:
DB  69 LGQVGRQLALIGDDINRRY 87

RESULT 11
Q9JK59
ID  Q9JK59 PRELIMINARY; PRT; 209 AA.
AC  Q9JK59;
DT  01-OCT-2000 (TrEMBLrel. 15, Created)
DT  01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT  01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE  BAK protein.
GN  Name=Bak;
OS  Rattus norvegicus (Rat).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX  NCBI_TaxID=10116;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=Sprague-Dawley;
RX  MEDLINE=22672518; PubMed=12787069;
RA  Itoh T., Itoh A., Pleasure D.;
RT  "Bcl-2-related protein family gene expression during oligodendroglial
RT  differentiation.";
RL  J. Neurochem. 85:1500-1512 (2003).
DR  EMBL; AF259504; AAF71760.1; -.
DR  HSP; Q16611; 1BLX.
DR  GO; GO:0042981; P:regulation of apoptosis; IEA.
DR  InterPro; IPR000712; BCL2_EH.
DR  InterPro; IPR002475; BCL2_family.
DR  Pfam; PF00452; Bcl-2; 1.
DR  SMART; SM00337; BCL; 1.
DR  PROSITE; PS00662; BCL2_FAMILY; 1.
DR  PROSITE; PS01080; BH1; UNKNOWN_1.
DR  PROSITE; PS01258; BH2; 1.
DR  PROSITE; PS01259; BH3; 1.
SQ  SEQUENCE 209 AA; 23153 MW; 2493B814B1972421 CRC64;

Query Match      90.2%; Score 92; DB 2; Length 209;
Best Local Similarity 89.5%; Pred. No. 4.9e-06;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY  2 MGQVGRQLAIIIGDDINRRY 20
   :|||||:|||||:
DB  69 LGQVGRQLALIGDDINRRY 87

RESULT 12
Q74116
ID  Q74116 PRELIMINARY; PRT; 264 AA.
AC  Q74116; Q6SEB1;
DT  05-JUL-2004 (TrEMBLrel. 27, Created)
DT  05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT  01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE  Hypothetical protein.
GN  OrderedLocusNames=LJ1752; ORFNames=LJ0_1752;
OC  Lactobacillus johnsonii NCC 533.
OC  Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC  Lactobacillus.
OX  NCBI_TaxID=257314;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=NCC 533;
RX  PubMed=14966310;
RA  Priddy R.D., Berger B., Desiere F., Vilanova D., Barretto C.,
RA  Pittet A.-C., Zwahlen M.-C., Rouvet M., Altermann E., Barrangou R.,
RA  Mollet B., Mercenier A., Kleenhamer T., Arigoni F., Schell M.A.;
RT  "The genome sequence of the probiotic intestinal bacterium

```

```
RT Lactobacillus johnsonii NCC 533.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:2512-2517(2004).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=NCC 533;
RX PubMed=15016546;
RA Ventura M., Canchaya C., Pridmore R.D., Brussow H.;
RT "The phages of Lactobacillus johnsonii NCC 533: comparative
RL genomics and transcription analysis.";
RL Virology 320:229-242(2004).
DR EMBL; AE017205; AA09524.1; -.
DR EMBL; AY459534; AAR27400.1; -.
DR InterPro; IPR003593; AAA ATPase.
DR InterPro; IPR002543; FtsK SpoIIIB.
DR Pfam; PF01580; FtsK SpoIIIE; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS0901; FTSK; 1.
KW ATP-binding.
SQ SEQUENCE 264 AA; 29627 MW; 006B84D619E84367 CRC64;

Query Match 49.0%; Score 50; DB 2; Length 264;
Best Local Similarity 45.0%; Pred. No. 21;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 1 TMGQVGRQLAIGDDINRY 20
Db 79 TTNQIARMLRLINENMNNRY 98

RESULT 13
AAR27400 PRELIMINARY; PRT; 264 AA.
AC AAR27400;
DT 25-MAR-2004 (TrEMBLrel. 27, Created)
DT 25-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 25-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN LJO 1752.
OS Lactobacillus johnsonii NCC 533.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus; Lactobacillus johnsonii.
OX NCBI_TaxID=257314;
[1]
RP SEQUENCE FROM N.A.
RX STRAIN=NCC 533;
RX PubMed=15016546;
RA Ventura M., Canchaya C., Pridmore R.D., Brussow H.;
RT "The phages of Lactobacillus johnsonii NCC 533: comparative
RL genomics and transcription analysis.";
RL Virology 320:229-242(2004).
DR EMBL; AY459534; AAR27400.1; -.
DR Hypothetical protein.
KW Hypothetical protein.
SQ SEQUENCE 264 AA; 29627 MW; 006B84D619E84367 CRC64;

Query Match 49.0%; Score 50; DB 2; Length 264;
Best Local Similarity 45.0%; Pred. No. 21;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 1 TMGQVGRQLAIGDDINRY 20
Db 79 TTNQIARMLRLINENMNNRY 98

RESULT 14
AA09524 PRELIMINARY; PRT; 264 AA.
AC AA09524;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN LJI752.
OS Lactobacillus johnsonii.

OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=33959;
[1]
RP SEQUENCE FROM N.A.
RX STRAIN=NCC 533;
RX PubMed=1496310;
RA Pridmore R.D., Rouvet M.-C., Altermann E., Barrangou R.,
RA Pittet A.-C., Zwahlen M., Klaenhammer T., Arigoni F., Schell M.A.;
RA Mollet B., Mercenier A., Klaenhammer T., Arigoni F., Schell M.A.;
RT "The genome sequence of the probiotic intestinal bacterium
RT Lactobacillus johnsonii NCC 533.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:2512-2517(2004).
DR EMBL; AE017205; AA09524.1; -.
KW Hypothetical protein.
SQ SEQUENCE 264 AA; 29627 MW; 006B84D619E84367 CRC64;

Query Match 49.0%; Score 50; DB 2; Length 264;
Best Local Similarity 45.0%; Pred. No. 21;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 1 TMGQVGRQLAIGDDINRY 20
Db 79 TTNQIARMLRLINENMNNRY 98

RESULT 15
K6P3_BACTN STANDARD; PRT; 336 AA.
AC Q8A2E9;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE 6-phosphofructokinase 3 (EC 2.7.1.11) (Phosphofructokinase 3)
DE (Phosphohexokinase 3).
GN Name=pfk3; OrderedLocNames=BT3356;
OS Bacteroides thetaiotaomicron.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=818;
[1]
RP SEQUENCE FROM N.A.
RX STRAIN=VPI-5482 / ATCC 29148;
RX MEDLINE=22550858; PubMed=12663928; DOI=10.1126/science.1080029;
RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
RA Chiang H.C., Hooper L.V., Gordon J.I.;
RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
RL Science 299:2074-2076(2003).
CC -|- CATALYTIC ACTIVITY: ATP + D-fructose 6-phosphate = ADP + D-
fructose 1,6-bisphosphate.
CC -|- PATHWAY: Key control step of glycolysis.
CC -|- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -|- SIMILARITY: Belongs to the phosphofructokinase family.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
CC EMBL; AE016940; AAO78462.1; -.
CC HSSP; P06998; 2PFK.
CC HAMAP; MF 00339; -.
CC InterPro; IPR000023; Ppf_rckinase.
CC Pfam; PF00365; PFK; 1.
CC PRINTS; PR00476; PHFRCTKINASE.
CC ProDom; PD000707; Ppf_rckinase; 1.
CC PROSITE; PS00433; PHOSPHOFRUCTOKINASE; FALSE_NEG.
CC Allosteric enzyme; ATP-binding; Complete proteome; Glycolysis; Kinase;
KW Magnesium; Transferase.
GN NP_BIND 20 24
FT NP_BIND 20 24 ATP (By similarity).
```

FT NP\_BIND 160 164 ATP (By similarity).  
 FT NP\_BIND 177 193 ATP (By similarity).  
 FT ACT\_SITE 133 133 Proton acceptor (By similarity).  
 FT BINDING 168 168 Substrate (By similarity).  
 FT BINDING 255 255 Substrate (By similarity).  
 FT BINDING 264 264 Substrate (By similarity).  
 SQ SEQUENCE 336 AA; 35853 MW; 990BAEF6B5BD5F79 CRC64;

Query Match 48.0%; Score 49; DB 1; Length 336;  
 Best Local Similarity 60.0%; Pred. No. 39;  
 Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 GOVGRGLAIIGDDIN 17  
 |||||:  
 |||||:  
 |||||:  
 Db 290 GQFGRMIALKGDDIS 304

Search completed: January 25, 2005, 10:10:33  
 Job time : 134 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 25, 2005, 10:06:01 ; Search time 28 seconds  
(without alignments)  
47.370 Million cell updates/sec

Title: US-09-828-870-39  
Perfect score: 104  
Sequence: 1 AADPLHEAMRAAGDEPETF 20

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A COMB.pcp.\*  
2: /cgn2\_6/ptodata/1/iaa/5B COMB.pcp.\*  
3: /cgn2\_6/ptodata/1/iaa/6A COMB.pcp.\*  
4: /cgn2\_6/ptodata/1/iaa/6B COMB.pcp.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pcp.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	104	100.0	20	3	US-09-236-385A-39
2	101	97.1	27	4	US-09-544-664B-24
3	101	97.1	192	1	US-08-798-897-5
4	101	97.1	192	1	US-08-798-897-6
5	101	97.1	192	2	US-08-798-897-5
6	101	97.1	192	2	US-08-798-897-6
7	101	97.1	193	1	US-08-798-897-3
8	101	97.1	193	1	US-08-798-897-4
9	101	97.1	193	2	US-08-798-523-3
10	101	97.1	193	2	US-08-798-523-4
11	101	97.1	193	4	US-09-155-327G-7
12	101	97.1	193	4	US-09-155-327G-9
13	101	97.1	333	4	US-09-155-327G-10
14	101	97.1	365	4	US-09-149-476-696
15	101	97.1	365	4	US-09-010-147B-24
16	82	78.8	16	4	US-09-544-664B-51
17	54	51.9	27	4	US-09-544-664B-12
18	54	51.9	190	1	US-08-081-448-2
19	54	51.9	190	2	US-08-470-670A-2
20	54	51.9	190	3	US-08-461-511A-2
21	54	51.9	190	3	US-09-271-014A-2
22	54	51.9	190	5	PCT-US94-07089-2
23	51	49.0	27	4	US-09-544-664B-13
24	51	49.0	49	1	US-08-321-071A-26
25	51	49.0	109	2	US-08-470-670A-11
26	51	49.0	109	3	US-08-461-511A-11
27	51	49.0	121	2	US-08-470-670A-15

28	51	49.0	121	3	US-08-461-511A-15	Sequence 15, Appl
29	51	49.0	170	1	US-08-081-448-8	Sequence 8, Appl
30	51	49.0	170	2	US-08-470-670A-9	Sequence 9, Appl
31	51	49.0	170	3	US-08-461-511A-9	Sequence 8, Appl
32	51	49.0	170	3	US-09-271-014A-8	Sequence 9, Appl
33	51	49.0	170	5	PCT-US94-07089-9	Sequence 1, Appl
34	51	49.0	225	3	US-09-101-519-1	Sequence 59, Appl
35	51	49.0	233	1	US-08-333-565-59	Sequence 6, Appl
36	51	49.0	233	1	US-08-081-448-6	Sequence 24, Appl
37	51	49.0	233	1	US-08-607-269-24	Sequence 14, Appl
38	51	49.0	233	1	US-08-471-058-14	Sequence 59, Appl
39	51	49.0	233	2	US-08-661-479-59	Sequence 7, Appl
40	51	49.0	233	2	US-08-470-670A-7	Sequence 14, Appl
41	51	49.0	233	3	US-08-471-057-14	Sequence 2, Appl
42	51	49.0	233	3	US-08-481-739-2	Sequence 2, Appl
43	51	49.0	233	3	US-09-167-921-2	Sequence 2, Appl
44	51	49.0	233	3	US-09-323-743-2	Sequence 7, Appl
45	51	49.0	233	3	US-08-461-511A-7	

ALIGNMENTS

RESULT 1  
US-09-236-385A-39  
; Sequence 39, Application US/09236385A  
; Patent No. 6221615  
; GENERAL INFORMATION:  
; APPLICANT: CHITTENDEN, Thomas D.; and  
; LUTZ, Robert J.  
; TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH  
; MODULATE APOPTOSIS  
; NUMBER OF SEQUENCES: 41  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hale and Dorr  
; STREET: 1455 Pennsylvania Avenue, N.W.  
; CITY: Washington  
; STATE: D.C.  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/236,385A  
; FILING DATE: 25-Jan-1999  
; CLASSIFICATION: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WIXON, HENRY N.  
; REGISTRATION NUMBER: 32,073  
; (C) ATTORNEY DOCKET NO. 104322.147CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-942-8400  
; TELEFAX: 202-942-8484  
; INFORMATION FOR SEQ ID NO: 39  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 39  
US-09-236-385A-39

Query Match 100.0%; Score 104; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 7.4e-11;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 AADPLHEAMRAAGDEPETF 20  
Db 1 AADPLHEAMRAAGDEPETF 20

RESULT 2  
US-09-544-664B-24  
; Sequence 24, Application US/09544664B  
; Patent No. 6713280  
; GENERAL INFORMATION:  
; APPLICANT: Huang, Ziwei  
; APPLICANT: Wang, Jialun  
; APPLICANT: Zhang, Zhijia  
; APPLICANT: Shan, Simei  
; APPLICANT: Lu, Zhixian  
; TITLE OF INVENTION: Enhancement of Peptide Cellular Uptake  
; FILE REFERENCE: 8321-68  
; CURRENT APPLICATION NUMBER: US/09/544,664B  
; CURRENT FILING DATE: 2000-04-06  
; PRIOR APPLICATION NUMBER: PCT/US00/09352  
; PRIOR FILING DATE: 2000-04-06  
; PRIOR APPLICATION NUMBER: 60/128,202  
; PRIOR FILING DATE: 1999-04-07  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 24  
; LENGTH: 27  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide  
; OTHER INFORMATION: segment from BH3 domain of a Bcl-2 superfamily  
; OTHER INFORMATION: polypeptide  
US-09-544-664B-24

Query Match 97.1%; Score 101; DB 4; Length 27;  
Best Local Similarity 95.0%; Pred. No. 3.3e-10;  
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADPLHEAMRAAGDEPETF 20  
Db 4 AADPLHQAAMRAAGDEPETF 23  
|||||:|||||

RESULT 3  
US-08-798-897-5  
; Sequence 5, Application US/08798897  
; Patent No. 5789201  
; GENERAL INFORMATION:  
; APPLICANT: Guastella, John  
; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2  
; TITLE OF INVENTION: Homologue  
; NUMBER OF SEQUENCES: 53  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
; STREET: 1100 New York Avenue, N.W., Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/798,897  
; FILING DATE: February 11, 1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Esmond, Robert W.  
; REGISTRATION NUMBER: 32,893  
; REFERENCE/DOCKET NUMBER: 1483.0140001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:

; LENGTH: 192 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-798-897-5  
Query Match 97.1%; Score 101; DB 1; Length 192;  
Best Local Similarity 95.0%; Pred. No. 3.1e-09;  
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AADPLHEAMRAAGDEPETF 20  
Db 37 AADPLHQAAMRAAGDEPETF 56  
|||||:|||||

RESULT 4  
US-08-798-897-6  
; Sequence 6, Application US/08798897  
; Patent No. 5789201  
; GENERAL INFORMATION:  
; APPLICANT: Guastella, John  
; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2  
; TITLE OF INVENTION: Homologue  
; NUMBER OF SEQUENCES: 53  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
; STREET: 1100 New York Avenue, N.W., Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/798,897  
; FILING DATE: February 11, 1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Esmond, Robert W.  
; REGISTRATION NUMBER: 32,893  
; REFERENCE/DOCKET NUMBER: 1483.0140001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 192 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-798-897-6

Query Match 97.1%; Score 101; DB 1; Length 192;  
Best Local Similarity 95.0%; Pred. No. 3.1e-09;  
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADPLHEAMRAAGDEPETF 20  
Db 37 AADPLHQAAMRAAGDEPETF 56  
|||||:|||||

RESULT 5  
US-08-978-523-5  
; Sequence 5, Application US/08978523  
; Patent No. 583229  
; GENERAL INFORMATION:  
; APPLICANT: Guastella, John  
; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2



;; TITLE OF INVENTION: Homologue  
;; NUMBER OF SEQUENCES: 53  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
;; STREET: 1100 New York Avenue, N.W., Suite 600  
;; CITY: Washington  
;; STATE: DC  
;; COUNTRY: USA  
;; ZIP: 20005  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/978,523  
;; FILING DATE: herewith  
;; CLASSIFICATION: 424  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/798,897  
;; FILING DATE: February 11, 1997  
;; CLASSIFICATION: 424  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Esmond, Robert W.  
;; REGISTRATION NUMBER: 32,893  
;; REFERENCE/DOCKET NUMBER: 1483.0140002  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 202-371-2600  
;; TELEFAX: 202-371-2540  
;; INFORMATION FOR SEQ ID NO: 5:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 192 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: not relevant  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; US-08-978-523-5

Query Match 97.1%; Score 101; DB 2; Length 192;  
Best Local Similarity 95.0%; Pred. No. 3.le-09;  
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADPLHEAMRAAGDEFETRF 20  
|||||:|||||  
Db 37 AADPLHQAMRAAGDEFETRF 56

RESULT 6  
US-08-978-523-6  
;; Sequence 6, Application US/08978523  
;; Patent No. 5883229  
;; GENERAL INFORMATION:  
;; APPLICANT: Guastella, John  
;; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2  
;; NUMBER OF SEQUENCES: 53  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
;; STREET: 1100 New York Avenue, N.W., Suite 600  
;; CITY: Washington  
;; STATE: DC  
;; COUNTRY: USA  
;; ZIP: 20005  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/978,523  
;; FILING DATE: herewith  
;; CLASSIFICATION: 424  
;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 08/798,897  
;; FILING DATE: February 11, 1997  
;; CLASSIFICATION: 424  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Esmond, Robert W.  
;; REGISTRATION NUMBER: 32,893  
;; REFERENCE/DOCKET NUMBER: 1483.0140002  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 202-371-2600  
;; TELEFAX: 202-371-2540  
;; INFORMATION FOR SEQ ID NO: 6:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 192 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: not relevant  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; US-08-978-523-6

Query Match 97.1%; Score 101; DB 2; Length 192;  
Best Local Similarity 95.0%; Pred. No. 3.le-09;  
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADPLHEAMRAAGDEFETRF 20  
|||||:|||||  
Db 37 AADPLHQAMRAAGDEFETRF 56

RESULT 7  
US-08-798-897-3  
;; Sequence 3, Application US/08798897  
;; Patent No. 5789201  
;; GENERAL INFORMATION:  
;; APPLICANT: Guastella, John  
;; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2  
;; NUMBER OF SEQUENCES: 53  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
;; STREET: 1100 New York Avenue, N.W., Suite 600  
;; CITY: Washington  
;; STATE: DC  
;; COUNTRY: USA  
;; ZIP: 20005  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/798,897  
;; FILING DATE: February 11, 1997  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Esmond, Robert W.  
;; REGISTRATION NUMBER: 32,893  
;; REFERENCE/DOCKET NUMBER: 1483.0140001  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 202-371-2600  
;; TELEFAX: 202-371-2540  
;; INFORMATION FOR SEQ ID NO: 3:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 193 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: not relevant  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; US-08-798-897-3

Query Match 97.1%; Score 101; DB 1; Length 193;  
Best Local Similarity 95.0%; Pred. No. 3.le-09;  
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADPLHEAMRAAGDEFETRF 20  
|||||:|||||  
Db 38 AADPLHQAMRAAGDEFETRF 57

RESULT 8  
US-08-798-897-4  
; Sequence 4, Application US/08798897  
; Patent No. 5789201  
; GENERAL INFORMATION:  
; APPLICANT: Guastella, John  
; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2  
; TITLE OF INVENTION: Homologue  
; NUMBER OF SEQUENCES: 53  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
; STREET: 1100 New York Avenue, N.W., Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM: disk  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/798,897  
; FILING DATE: February 11, 1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Esmond, Robert W.  
; REGISTRATION NUMBER: 32,893  
; REFERENCE/DOCKET NUMBER: 1483.0140001  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 193 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-798-897-4

Query Match 97.1%; Score 101; DB 1; Length 193;  
Best Local Similarity 95.0%; Pred. No. 3.1e-09;  
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADPLHEAMRAAGDEFETRF 20  
|||||:|||||  
Db 38 AADPLHQAMRAAGDEFETRF 57

RESULT 9  
US-08-978-523-3  
; Sequence 3, Application US/08978523  
; Patent No. 5883229  
; GENERAL INFORMATION:  
; APPLICANT: Guastella, John  
; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2  
; TITLE OF INVENTION: Homologue  
; NUMBER OF SEQUENCES: 53  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
; STREET: 1100 New York Avenue, N.W., Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM: disk  
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/978,523  
; FILING DATE: herewith  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/798,897  
; FILING DATE: February 11, 1997  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Esmond, Robert W.  
; REGISTRATION NUMBER: 32,893  
; REFERENCE/DOCKET NUMBER: 1483.0140002  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 193 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-978-523-3

Query Match 97.1%; Score 101; DB 2; Length 193;  
Best Local Similarity 95.0%; Pred. No. 3.1e-09;  
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADPLHEAMRAAGDEFETRF 20  
|||||:|||||  
Db 38 AADPLHQAMRAAGDEFETRF 57

RESULT 10  
US-08-978-523-4  
; Sequence 4, Application US/08978523  
; Patent No. 5883229  
; GENERAL INFORMATION:  
; APPLICANT: Guastella, John  
; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2  
; TITLE OF INVENTION: Homologue  
; NUMBER OF SEQUENCES: 53  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
; STREET: 1100 New York Avenue, N.W., Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM: disk  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/978,523  
; FILING DATE: herewith  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/798,897  
; FILING DATE: February 11, 1997  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Esmond, Robert W.  
; REGISTRATION NUMBER: 32,893  
; REFERENCE/DOCKET NUMBER: 1483.0140002  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 4:

; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/978,523  
; FILING DATE: herewith  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/798,897  
; FILING DATE: February 11, 1997  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Esmond, Robert W.  
; REGISTRATION NUMBER: 32,893  
; REFERENCE/DOCKET NUMBER: 1483.0140002  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 193 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-978-523-4

Query Match 97.1%; Score 101; DB 2; Length 193;  
Best Local Similarity 95.0%; Pred. No. 3.le-09;

Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADPLHQAAMRAAGDEFETRF 20

Db 38 AADPLHQAAMRAAGDEFETRF 57

#### RESULT 11

US-09-155-327G-7

; Sequence 7, Application US/09155327G

; Patent No. 6790637

; GENERAL INFORMATION:

; APPLICANT: AMRAD Operations Pty Ltd

; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-2, BELONGS TO THE bcl-2  
; FILE REFERENCE: 2096584

; CURRENT APPLICATION NUMBER: US/09/155,327G

; CURRENT FILING DATE: 1999-03-29

; PRIOR APPLICATION NUMBER: PN8965

; PRIOR FILING DATE: 1996-03-27

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 7

; LENGTH: 193

; TYPE: PRT

; ORGANISM: HUMAN

US-09-155-327G-7

Query Match 97.1%; Score 101; DB 4; Length 193;

Best Local Similarity 95.0%; Pred. No. 3.le-09;

Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADPLHQAAMRAAGDEFETRF 20

Db 38 AADPLHQAAMRAAGDEFETRF 57

#### RESULT 12

US-09-155-327G-9

; Sequence 9, Application US/09155327G

; Patent No. 6790637

; GENERAL INFORMATION:

; APPLICANT: AMRAD Operations Pty Ltd

; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-2, BELONGS TO THE bcl-2  
; FILE REFERENCE: 2096584

; CURRENT APPLICATION NUMBER: US/09/155,327G

; CURRENT FILING DATE: 1999-03-29

; PRIOR APPLICATION NUMBER: PN8965

; PRIOR FILING DATE: 1996-03-27

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 9

; LENGTH: 193

; TYPE: PRT

; ORGANISM: Mouse

US-09-155-327G-9

Query Match 97.1%; Score 101; DB 4; Length 193;

Best Local Similarity 95.0%; Pred. No. 3.le-09;

Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADPLHQAAMRAAGDEFETRF 20

Db 38 AADPLHQAAMRAAGDEFETRF 57

#### RESULT 13

US-09-155-327G-10

; Sequence 10, Application US/09155327G

; Patent No. 6790637

; GENERAL INFORMATION:

; APPLICANT: AMRAD Operations Pty Ltd

; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-2, BELONGS TO THE bcl-2  
; FILE REFERENCE: 2096584

; CURRENT APPLICATION NUMBER: US/09/155,327G

; CURRENT FILING DATE: 1999-03-29

; PRIOR APPLICATION NUMBER: PN8965

; PRIOR FILING DATE: 1996-03-27

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 10

; LENGTH: 333

; TYPE: PRT

; ORGANISM: murine

US-09-155-327G-10

Query Match 97.1%; Score 101; DB 4; Length 333;

Best Local Similarity 95.0%; Pred. No. 5.9e-09;

Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADPLHQAAMRAAGDEFETRF 20

Db 38 AADPLHQAAMRAAGDEFETRF 57

#### RESULT 14

US-09-149-476-696

; Sequence 696, Application US/09149476

; Patent No. 6420526

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: 186 Human Secreted proteins

; FILE REFERENCE: P2002P1

; CURRENT APPLICATION NUMBER: US/09/149,476

; CURRENT FILING DATE: 1998-09-08

; EARLIER APPLICATION NUMBER: PCT/US98/04493

; EARLIER FILING DATE: 1998-03-06

; EARLIER APPLICATION NUMBER: 60/040,162

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,333

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/038,621

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,626

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,334

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,336

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,163

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/047,600

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,615

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,597

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,502

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,633

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,583

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,617



EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,887  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,908  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/048,964  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/057,650  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/056,884  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/057,669  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/049,610  
EARLIER FILING DATE: 1997-06-13  
EARLIER APPLICATION NUMBER: 60/061,060  
EARLIER FILING DATE: 1997-10-02

Query Match 97.1%; Score 101; DB 4; Length 365;  
Best Local Similarity 95.0%; Pred. No. 6.5e-09;  
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADPLHEAMRAAGDEFETRF 20  
|||||:|||||  
Db 38 AADPLHQMRAAGDEFETRF 57

## RESULT 15

US-09-010-147B-24  
Sequence 24, Application US/09010147B  
Patent No. 6653445  
GENERAL INFORMATION:  
APPLICANT: Ni et al.  
TITLE OF INVENTION: Human Proteins  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: MD  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC  
compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/010,147B  
FILING DATE: 12-No. 6653445-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/034,205  
FILING DATE: 21-JAN-1997  
APPLICATION NUMBER: US 60/034,204  
FILING DATE: 21-JAN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Jonathan L. Klein  
REGISTRATION NUMBER: 41,119  
REFERENCE/DOCKET NUMBER: PF353  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-309-8504  
TELEFAX: 301-309-8439  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 365 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 24:

US-09-010-147B-24

Query Match 97.1%; Score 101; DB 4; Length 365;  
Best Local Similarity 95.0%; Pred. No. 6.5e-09;  
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADPLHEAMRAAGDEFETRF 20  
|||||:|||||  
Db 38 AADPLHQMRAAGDEFETRF 57

Search completed: January 25, 2005, 10:15:36  
Job time : 29 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 25, 2005, 10:10:46 ; Search time 97.5 Seconds  
(without alignments)  
74.111 Million cell updates/sec

Title: US-09-828-870-39

Perfect score: 104

Sequence: 1 AADPLHEAMRAAGDEPETRF 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA:\*

1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*  
17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*  
19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	104	100.0	20	11	US-09-828-870-39
2	101	97.1	193	9	US-09-925-674A-7
3	101	97.1	193	9	US-09-925-674A-9
4	101	97.1	193	16	US-10-450-366-6
5	101	97.1	365	10	US-09-809-391-696
6	101	97.1	365	10	US-09-882-171-696
7	101	97.1	365	14	US-10-164-861-696
8	74	71.2	15	9	US-09-738-396-16
9	67	64.4	228	16	US-10-659-705-2
10	56	53.8	179	14	US-10-402-017-6
11	56	53.8	199	14	US-10-402-017-8
12	56	53.8	219	14	US-10-402-017-10
13	54	51.9	190	9	US-09-952-278-2

14	51.9	229	16	US-10-659-705-7	Sequence 7, Appli
15	51.0	152	14	US-10-158-769-2	Sequence 2, Appli
16	51.0	152	17	US-10-729-156-2	Sequence 2, Appli
17	49.0	25	14	US-10-071-174-29	Sequence 29, Appli
18	49.0	170	9	US-09-952-278-8	Sequence 8, Appli
19	49.0	170	15	US-10-003-632C-7	Sequence 7, Appli
20	49.0	185	9	US-09-864-761-40954	Sequence 40954, A
21	49.0	212	14	US-10-169-223-14	Sequence 14, Appli
22	49.0	219	14	US-10-402-017-12	Sequence 12, Appli
23	49.0	233	9	US-09-734-846-2	Sequence 2, Appli
24	49.0	233	9	US-09-952-278-6	Sequence 6, Appli
25	49.0	233	14	US-10-101-482-14	Sequence 14, Appli
26	49.0	233	14	US-10-072-830-4	Sequence 4, Appli
27	49.0	233	14	US-10-169-223-10	Sequence 10, Appli
28	49.0	233	14	US-10-302-262-2	Sequence 2, Appli
29	49.0	233	14	US-10-116-275-171	Sequence 171, App
30	49.0	233	14	US-10-402-017-4	Sequence 4, Appli
31	49.0	233	16	US-10-450-366-5	Sequence 5, Appli
32	49.0	233	16	US-10-659-705-8	Sequence 8, Appli
33	49.0	233	17	US-10-825-282-48	Sequence 48, Appli
34	49.0	235	14	US-10-208-155-2	Sequence 2, Appli
35	49.0	411	16	US-10-792-517-2	Sequence 8, Appli
36	49.0	485	16	US-10-792-517-8	Sequence 3, Appli
37	48.1	233	16	US-10-659-705-3	Sequence 15, Appli
38	46.2	15	9	US-09-738-396-15	Sequence 135064,
39	46.2	109	16	US-10-437-963-135064	Sequence 167244,
40	46.2	560	15	US-10-424-599-167244	Sequence 12155, A
41	46.2	942	14	US-10-156-761-12155	Sequence 7, Appli
42	45.2	205	8	US-08-726-211-7	Sequence 23, Appli
43	45.2	205	9	US-09-952-278-4	Sequence 7, Appli
44	45.2	205	14	US-10-053-645A-23	Sequence 7, Appli
45	45.2	205	14	US-10-387-961A-7	

#### ALIGNMENTS

#### RESULT 1

US-09-828-870-39  
; Sequence 39, Application US/09828870  
; Publication No. US20040054129A1  
; GENERAL INFORMATION:  
; APPLICANT: CHITTENDEN, Thomas D.; and  
; LUTZ, Robert J.  
; TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH  
; MODULATE APOPTOSIS  
; NUMBER OF SEQUENCES: 41  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hale and Dorr  
; STREET: 1455 Pennsylvania Avenue, N.W.  
; CITY: Washington  
; STATE: D.C.  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/828,870  
; FILING DATE: 10-Apr-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/236,385  
; FILING DATE: 25-JANUARY-1999  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WIXON, HENRY N.  
; REGISTRATION NUMBER: 32,073  
; (C) ATTORNEY DOCKET NO. 104322.147CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-942-8400  
; TELEFAX: 202-942-8484  
; INFORMATION FOR SEQ ID NO: 39

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 39  
US-09-828-870-39

Query Match 100.0%; Score 104; DB 11; Length 20;

Best Local Similarity 100.0%; Pred. No. 6.6e-10;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADPLHEAMRAAGDEFETRF 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1 AADPLHEAMRAAGDEFETRF 20

RESULT 2  
US-09-925-674A-7  
; Sequence 7, Application US/09925674A  
; Patent No. US20020119943A1  
; GENERAL INFORMATION:  
; APPLICANT: AMRAD Operations Pty Ltd  
; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-w, BELONGS TO THE bcl-2  
; FAMILY OF APOPTOSIS-CONTROLLING GENES  
; FILE REFERENCE: 11686A  
; CURRENT APPLICATION NUMBER: US/09/925,674A  
; CURRENT FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: 09/925,674  
; PRIOR FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: PN8965  
; PRIOR FILING DATE: 1996-03-27  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 193  
; TYPE: PRT  
; ORGANISM: HUMAN  
US-09-925-674A-7

Query Match 97.1%; Score 101; DB 9; Length 193;

Best Local Similarity 95.0%; Pred. No. 2.6e-08;  
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADPLHEAMRAAGDEFETRF 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 38 AADPLHQAMRAAGDEFETRF 57

RESULT 3  
US-09-925-674A-9  
; Sequence 9, Application US/09925674A  
; Patent No. US20020119943A1  
; GENERAL INFORMATION:  
; APPLICANT: AMRAD Operations Pty Ltd  
; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-w, BELONGS TO THE bcl-2  
; FAMILY OF APOPTOSIS-CONTROLLING GENES  
; FILE REFERENCE: 11686A  
; CURRENT APPLICATION NUMBER: US/09/925,674A  
; CURRENT FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: 09/925,674  
; PRIOR FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: PN8965  
; PRIOR FILING DATE: 1996-03-27  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 193  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-925-674A-9

Query Match 97.1%; Score 101; DB 9; Length 193;

Best Local Similarity 95.0%; Pred. No. 2.6e-08;  
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADPLHEAMRAAGDEFETRF 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 38 AADPLHQAMRAAGDEFETRF 57

RESULT 4  
US-10-450-366-6  
; Sequence 6, Application US/10450366  
; Publication No. US20040115667A1  
; GENERAL INFORMATION:  
; APPLICANT: Tschopp, Jörg  
; APPLICANT: Hoffmann, Kay  
; TITLE OF INVENTION: DNA-Sequences, Which Code For An Apoptosis Signal Transduction P:  
; FILE REFERENCE: 11436\*3  
; CURRENT APPLICATION NUMBER: US/10/450,366  
; CURRENT FILING DATE: 2003-11-21  
; PRIOR APPLICATION NUMBER: PCT/EP01/14597  
; PRIOR FILING DATE: 2001-12-12  
; PRIOR APPLICATION NUMBER: DE 100 61 766.2  
; PRIOR FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: DE 101 00 280.7  
; PRIOR FILING DATE: 2001-01-04  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 6  
; LENGTH: 193  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Human Bcl-W  
US-10-450-366-6

Query Match 97.1%; Score 101; DB 16; Length 193;

Best Local Similarity 95.0%; Pred. No. 2.6e-08;  
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADPLHEAMRAAGDEFETRF 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 38 AADPLHQAMRAAGDEFETRF 57

RESULT 5  
US-09-809-391-696  
; Sequence 696, Application US/09809391  
; Publication No. US20030049618A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: 186 Human Secreted proteins  
; FILE REFERENCE: PZ002P2  
; CURRENT APPLICATION NUMBER: US/09/809,391  
; CURRENT FILING DATE: 2001-03-16  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 761  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 696  
; LENGTH: 365  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-809-391-696

Query Match 97.1%; Score 101; DB 10; Length 365;

Best Local Similarity 95.0%; Pred. No. 5.2e-08;  
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADPLHEAMRAAGDEFETRF 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 38 AADPLHQAMRAAGDEFETRF 57

RESULT 6



US-09-882-171-696  
; Sequence 696, Application US/09882171  
; Publication No. US20030175858A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: 186 Human Secreted proteins  
; FILE REFERENCE: P2002P2  
; CURRENT APPLICATION NUMBER: US/09/882,171  
; CURRENT FILING DATE: 2001-06-18  
; PRIOR APPLICATION NUMBER: 09/809,391  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 09/149,476  
; PRIOR FILING DATE: 1998-09-08  
; PRIOR APPLICATION NUMBER: PCT/US98/04493  
; PRIOR FILING DATE: 1998-03-06  
; PRIOR APPLICATION NUMBER: 60/040,162  
; PRIOR FILING DATE: 1997-03-07  
; PRIOR APPLICATION NUMBER: 60/040,333  
; PRIOR FILING DATE: 1997-03-07  
; PRIOR APPLICATION NUMBER: 60/038,621  
; PRIOR FILING DATE: 1997-03-07  
; PRIOR APPLICATION NUMBER: 60/040,626  
; PRIOR FILING DATE: 1997-03-07  
; PRIOR APPLICATION NUMBER: 60/040,334  
; PRIOR FILING DATE: 1997-03-07  
; PRIOR APPLICATION NUMBER: 60/040,336  
; PRIOR FILING DATE: 1997-03-07  
; PRIOR APPLICATION NUMBER: 60/040,163  
; PRIOR FILING DATE: 1997-03-07  
; PRIOR APPLICATION NUMBER: 60/047,600  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,615  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,597  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,502  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,633  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,583  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,617  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,618  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,503  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,592  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,581  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,584  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,500  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,587  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,492  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,598  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,613  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,582  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,596  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,612  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,632  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,601  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/043,580  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,568  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,314  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,569  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,311  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,671  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,674  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,669  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,312  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,313  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,672  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,315  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/048,974  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/056,886  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,877  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,889  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,893  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,630  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,878  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,662  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,872  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,882  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,637  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,903  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,888  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,879  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,880  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,894  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,911  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,636  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,874  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,910  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,864  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,631  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,845  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,892  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/057,761

; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/047,595  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,599  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,588  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,585  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,586  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,590  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,594  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,589  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,593  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,614  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/043,578  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,576  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/047,501  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/043,670  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/056,632  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,664  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,876  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,881  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,909  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,875  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,862  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,887  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,908  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/048,964  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/057,650  
; PRIOR FILING DATE: 1997-09-05  
; PRIOR APPLICATION NUMBER: 60/056,884  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/057,669  
; PRIOR FILING DATE: 1997-09-05

Query Match 97.1%; Score 101; DB 10; Length 365;  
Best Local Similarity 95.0%; Pred. No. 5.2e-08;  
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADPLHEAMRAAGDEFETRF 20  
|||:|||||  
Db 38 AADPLHQAMRAAGDEFETRF 57

RESULT 7  
US-10-164-861-696  
; Sequence 696, Application US/10164861  
; Publication No. US20030225248A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 186 Human Secreted proteins  
; FILE REFERENCE: PZ002P1

; CURRENT APPLICATION NUMBER: US/10/164,861  
; CURRENT FILING DATE: 2002-06-10  
; PRIOR APPLICATION NUMBER: US/09/149,476  
; PRIOR FILING DATE: 1998-09-08  
; PRIOR APPLICATION NUMBER: PCT/US98/04493  
; PRIOR FILING DATE: 1998-03-06  
; NUMBER OF SEQ ID NOS: 757  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 696  
; LENGTH: 365  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-164-861-696

Query Match 97.1%; Score 101; DB 14; Length 365;  
Best Local Similarity 95.0%; Pred. No. 5.2e-08;  
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADPLHEAMRAAGDEFETRF 20  
|||:|||||  
Db 38 AADPLHQAMRAAGDEFETRF 57

RESULT 8  
US-09-738-396-16  
; Sequence 16, Application US/09738396  
; Patent No. US20010029013A1  
; GENERAL INFORMATION:  
; APPLICANT: Reed, John C.  
; TITLE OF INVENTION: BCL-G Polypeptides, Encoding Nucleic Acids and Methods  
; FILE REFERENCE: P-LJ 4450  
; CURRENT APPLICATION NUMBER: US/09/738,396  
; CURRENT FILING DATE: 2000-12-14  
; PRIOR APPLICATION NUMBER: US 09/461,641  
; PRIOR FILING DATE: 1999-12-14  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 16  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-738-396-16

Query Match 71.2%; Score 74; DB 9; Length 15;  
Best Local Similarity 93.3%; Pred. No. 3.9e-05;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 LHEAMRAAGDEFETR 19  
|||:|||||  
Db 1 LHQAMRAAGDEFETR 15

RESULT 9  
US-10-659-705-2  
; Sequence 2, Application US/10659705  
; Publication No. US20040117867A1  
; GENERAL INFORMATION:  
; APPLICANT: Look, A. Thomas  
; APPLICANT: Langenau, David M.  
; TITLE OF INVENTION: Transgenic Cancer Models in Fish  
; FILE REFERENCE: 112706.123  
; CURRENT APPLICATION NUMBER: US/10/659,705  
; CURRENT FILING DATE: 2003-09-11  
; PRIOR APPLICATION NUMBER: US 60/409,585  
; PRIOR FILING DATE: 2002-09-11  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 228  
; TYPE: PRT  
; ORGANISM: Artificial Sequence

; FEATURE:  
; OTHER INFORMATION: BCL2 proteins  
US-10-659-705-2

Query Match 54.4%; Score 67; DB 16; Length 228;  
Best Local Similarity 73.7%; Pred. No. 0.011;  
Matches 14; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 AADPLHEAMRAAGDEFETR 19  
| : |||||  
Db 73 ASCALHSAMRAAGDEFEE 91

RESULT 10  
US-10-402-017-6

; Sequence 6, Application US/10402017  
; Publication No. US20030219871A1

; GENERAL INFORMATION:

; APPLICANT: Barbara ENENKEL, Heiko MEENTS and Martin FUSSENEGGER

; TITLE OF INVENTION: Host cells having improved survival properties and methods to gen

; TITLE OF INVENTION: such cells

; FILE REFERENCE: Case 1/1314

; CURRENT APPLICATION NUMBER: US/10/402,017

; PRIOR FILING DATE: 2003-03-28

; PRIOR APPLICATION NUMBER: US 60/369,307

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 6

; LENGTH: 179

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Deletion mutant of SEQ ID NO:4 (del26-83)

US-10-402-017-6

Query Match 53.8%; Score 56; DB 14; Length 179;  
Best Local Similarity 55.0%; Pred. No. 0.54;  
Matches 11; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 AADPLHEAMRAAGDEFETR 20  
| : |||||  
Db 28 AAAAVKQALREAGDEFELRY 47

RESULT 11

US-10-402-017-8

; Sequence 8, Application US/10402017  
; Publication No. US20030219871A1

; GENERAL INFORMATION:

; APPLICANT: Barbara ENENKEL, Heiko MEENTS and Martin FUSSENEGGER

; TITLE OF INVENTION: Host cells having improved survival properties and methods to gen

; TITLE OF INVENTION: such cells

; FILE REFERENCE: Case 1/1314

; CURRENT APPLICATION NUMBER: US/10/402,017

; PRIOR FILING DATE: 2003-03-28

; PRIOR APPLICATION NUMBER: US 60/369,307

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 8

; LENGTH: 199

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Deletion mutant of SEQ ID NO:4 (del46-83)

US-10-402-017-8

Query Match 53.8%; Score 56; DB 14; Length 199;  
Best Local Similarity 55.0%; Pred. No. 0.6;  
Matches 11; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 AADPLHEAMRAAGDEFETR 20

Db 48 AAAAVKQALREAGDEFELRY 67  
| : |||||

RESULT 12

US-10-402-017-10

; Sequence 10, Application US/10402017  
; Publication No. US20030219871A1

; GENERAL INFORMATION:

; APPLICANT: Barbara ENENKEL, Heiko MEENTS and Martin FUSSENEGGER

; TITLE OF INVENTION: Host cells having improved survival properties and methods to ge

; TITLE OF INVENTION: such cells

; FILE REFERENCE: Case 1/1314

; CURRENT APPLICATION NUMBER: US/10/402,017

; PRIOR FILING DATE: 2003-03-28

; PRIOR APPLICATION NUMBER: US 60/369,307

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 10

; LENGTH: 219

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Deletion mutant of SEQ ID NO:4 (del66-83)

US-10-402-017-10

Query Match 53.8%; Score 56; DB 14; Length 219;  
Best Local Similarity 55.0%; Pred. No. 0.67;  
Matches 11; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 AADPLHEAMRAAGDEFETR 20  
| : |||||  
Db 68 AAAAVKQALREAGDEFELRY 87

RESULT 13

US-09-952-278-2

; Sequence 2, Application US/09952278  
; Patent No. US20020137182A1

; GENERAL INFORMATION:

; APPLICANT: Thompson, Craig B.  
Boise, Lawrence H.

; TITLE OF INVENTION: Vertebrate Apoptosis Gene:  
Compositions and Methods

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Arnold, White & Durkee

; STREET: 321 No. US20020137182Alth Clark Street, Suite 800

; CITY: Chicago

; STATE: IL

; COUNTRY: USA

; ZIP: 60610

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/952,278

; FILING DATE: 12-Sep-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/081,448

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: No. US20020137182Althrup, Thomas E.

; REGISTRATION NUMBER: 33,268

; REFERENCE/DOCKET NUMBER: ARCD090

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312-744-0090

; TELEFAX: 312-755-4489

; INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:  
LENGTH: 190 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-952-278-2

Query Match 51.9%; Score 54; DB 9; Length 190;  
Best Local Similarity 52.8%; Pred. No. 1.2;  
Matches 10; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 ADPLHEAMRAAGDEFEFTRF 20  
DB 79 ASDVRQALRDAGDEFEFLRY 97

RESULT 14  
US-10-659-705-7  
Sequence 7, Application US/10659705  
Publication No. US20040117867A1  
GENERAL INFORMATION:  
APPLICANT: Look, A. Thomas  
TITLE OF INVENTION: Transgenic Cancer Models in Fish  
FILE REFERENCE: 112706.123  
CURRENT APPLICATION NUMBER: US/10/659,705  
CURRENT FILING DATE: 2003-09-11  
PRIOR APPLICATION NUMBER: US 60/409,585  
PRIOR FILING DATE: 2002-09-11  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 7  
LENGTH: 229  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: BCL2 proteins  
US-10-659-705-7

Query Match 51.9%; Score 54; DB 16; Length 229;  
Best Local Similarity 52.6%; Pred. No. 1.5;  
Matches 10; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 ADPLHEAMRAAGDEFEFTRF 20  
DB 79 ASDVRQALRDAGDEFEFLRY 97

RESULT 15  
US-10-158-769-2  
Sequence 2, Application US/10158769  
Publication No. US20030008924A1  
GENERAL INFORMATION:  
APPLICANT: Yang, Dajun  
TITLE OF INVENTION: Small Molecule Antagonists of BCL-2 Family Protein  
FILE REFERENCE: UM-07232  
CURRENT APPLICATION NUMBER: US/10/158,769  
CURRENT FILING DATE: 2002-09-09  
PRIOR APPLICATION NUMBER: 60/293,983  
PRIOR FILING DATE: 2001-05-30  
NUMBER OF SEQ ID NOS: 3  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 2  
LENGTH: 152  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic  
US-10-158-769-2

Query Match 51.0%; Score 53; DB 14; Length 152;

Best Local Similarity 47.4%; Pred. No. 1.4;  
Matches 9; Conservative 6; Mismatches 4; Indels 0; Gaps 0;  
QY 2 ADPLHEAMRAAGDEFEFTRF 20  
DB 39 SEAVKQALREAGDEFEFLRY 57

Search completed: January 25, 2005, 10:31:00  
Job time : 97.5 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 25, 2005, 10:06:01 ; Search time 117.5 Seconds  
(without alignments)

61.060 Million cell updates/sec

Title: US-09-828-870-39

Perfect score: 104

Sequence: 1 AADPLHEAMRAAGDEPETF 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_23Sep04:\*

1: Geneseq1980s:\*

2: Geneseq1990s:\*

3: Geneseq2000s:\*

4: Geneseq2001s:\*

5: Geneseq2002s:\*

6: Geneseq2003as:\*

7: Geneseq2003bs:\*

8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	104	100.0	20	5	Aau77894 Bcl-w pep
2	104	100.0	20	8	Adk14726 Bcl-2 rel
3	101	97.1	27	3	Aab37024 Bcl2 poly
4	101	97.1	168	2	Aaw36048 Mouse bcl
5	101	97.1	183	8	Adp88350 Derivat
6	101	97.1	192	2	Aaw97394 Mammalian
7	101	97.1	192	2	Aaw97393 Protein s
8	101	97.1	192	2	Aay05533 Mouse bcl
9	101	97.1	193	2	Aaw36047 Human bcl
10	101	97.1	193	2	Aaw61392 Human bcl
11	101	97.1	193	2	Aaw61391 Rat bcl-y
12	101	97.1	193	2	Aaw97392 The human
13	101	97.1	193	2	Aaw97391 The rat b
14	101	97.1	193	2	Aay05530 Human bcl
15	101	97.1	193	2	Aay05532 Human bcl
16	101	97.1	193	2	Aay05531 Mouse bcl
17	101	97.1	193	7	Adk46742 Human Pro
18	101	97.1	193	8	Adp88349 Human bcl
19	101	97.1	365	2	Aaw59884 Amino aci
20	101	97.1	365	5	Abg95556 Human nov
21	101	97.1	365	6	Abc34750 Fragment
22	101	97.1	365	7	Adi23411 Novel hum
23	101	97.1	365	8	Adh74413 Human sec
24	82	78.8	16	3	Aab37051 Bcl2 poly
25	74	71.2	15	4	Aab85177 BH3 domai

#### ALIGNMENTS

RESULT 1

AAU77894

ID AAU77894 standard; peptide; 20 AA.

XX AC

XX AAU77894;

DT 05-JUN-2002 (first entry)

DE Bcl-w peptide tested for ability to block GD domain interactions.

XX GD domain; apoptosis; interaction with Bcl-XL; cell killing function;

KW bak; cell death regulatory molecule; autoimmune disease; cancer; bcl-w.

XX Unidentified.

XX US6221615-B1.

XX 24-APR-2001.

XX 25-JAN-1999; 99US-00236385.

XX 12-MAY-1995; 95US-00440391.

XX 08-AUG-1997; 97US-00908597.

XX (APOP-) APOPTOSIS TECHNOLOGY INC.

XX Chittenden TD, Lutz RJ;

XX WPI; 2002-234950/29.

XX Identifying agents (e.g. modulators of apoptosis) capable of modulating

GD domain mediated heterodimerization or homodimerization comprises

carrying out a heterodimerization or homodimerization assay.

XX Disclosure; Col 6; 37pp; English.

XX The present invention relates to novel peptides, designated GD domains,

which are capable of modulating apoptosis. The GD domains are essential

for Bak's interaction with Bcl-XL, and to Bak's cell killing function.

XX The GD domains mediate key protein/protein interactions with multiple

cell death regulatory molecules. Also described are methods of

identifying agonists or antagonists of GD domains. The methods are useful

for identifying agents capable of modulating GD domain mediated

heterodimerisation or homodimerisation. The methods are particularly

useful in drug screening and design, e.g. for identifying agents for

treating autoimmune disease or cancer, or for identifying modulators of

apoptosis. The present sequence represents a peptide tested for it's

ability to block GD domain-mediated interactions

Aao18223 Human Bcl  
Adh52635 Chinese h  
Adh52637 Chinese h  
Adh52639 Chinese h  
Aab37012 Bcl2 poly  
Aar68884 Chicken l  
Aag79760 Bcl-XL. 4  
Adk65102 PP1c-inte  
Aab37013 Bcl2 poly  
Aar68888 Human thy  
Aae37656 Bcl2 rela  
Adl69727 Human Bcl  
Abb42045 Peptide #  
Aam35847 Peptide #  
Abb25656 Protein #  
Aam75738 Human bon  
Aam62926 Human bra  
Abg57476 Human liv  
Abg45220 Human pep  
Aab20495 Human Bcl

65.5 63.0 190 5 AAO18223  
56 53.8 179 8 ADH52635  
56 53.8 199 8 ADH52637  
56 53.8 219 8 ADH52639  
54 51.9 27 3 AAB37012  
54 51.9 190 2 AAR68884  
53 51.0 152 6 AAG79760  
51 49.0 23 8 ADK65102  
51 49.0 27 3 AAB37013  
51 49.0 170 2 AAR68888  
51 49.0 170 6 AAE37656  
51 49.0 170 8 ADL69727  
51 49.0 185 4 ABB42045  
51 49.0 185 4 AAM35847  
51 49.0 185 4 ABB25656  
51 49.0 185 4 AAM75738  
51 49.0 185 4 AAM62926  
51 49.0 185 4 ABG57476  
51 49.0 185 5 ABG45220  
51 49.0 212 4 AAB20495

XX SQ Sequence 20 AA;  
Query Match 100.0%; Score 104; DB 5; Length 20;  
Best Local Similarity 100.0%; Pred. No. 4.4e-10;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADPLHEAMRAAGDEFETRF 20  
DB 1 AADPLHEAMRAAGDEFETRF 20  
|||||

RESULT 2  
ADKL4726  
ID ADKL4726 standard; peptide; 20 AA.  
XX AC ADKL4726;  
XX DT 03-JUN-2004 (first entry)  
XX DE BCL-2 related gene GD domain peptide seqid 39.  
XX KW anti-HIV; dermatological; immunosuppressive; antiinflammatory;  
KW antirheumatic; antiarthritic; GD domain peptide; apoptosis;  
KW protein domain; GD domain; bcl-2 related gene; Bak; cell death;  
KW immunocrossreactive protein; degenerative disorder;  
KW cell proliferation disorder; cell death disorder; autoimmune disease;  
KW systemic lupus erythematosus; SLE; rheumatoid arthritis;  
KW acquired immunodeficiency syndrome; AIDS.  
XX OS Unidentified.  
XX PN US2004054129-A1.  
XX PD 18-MAR-2004.  
XX PF 10-APR-2001; 2001US-00828870.  
XX PR 12-MAY-1995; 95US-00440391.  
XX PR 08-AUG-1997; 97US-00908597.  
XX PR 25-JAN-1999; 99US-00236385.  
XX (APOF-) APOPTOSIS TECHNOLOGY INC.  
XX PA Chittenden TD, Lutz RJ;  
XX PI WPI; 2004-247780/23.  
XX DR Novel isolated and purified peptide comprising GD domain, useful for  
PT treating degenerative disease e.g., rheumatoid arthritis.  
XX PS Disclosure; SEQ ID NO 39; 38pp; English.  
XX

The invention describes an isolated and purified peptide (I) comprising  
CC unrecognised protein domain (GD domain) isolated from the bcl-2 related  
CC gene Bak that can induce cell death. (I) is useful for identifying an  
CC agent capable of modulating GD domain radiated heterodimerisation or  
CC homodimerisation. (iv) is useful for screening a cDNA expression library  
CC for clones comprising DNA inserts encoding immunocrossreactive proteins  
CC (claimed). An anti-(I)-antibody, its mimetics, fragments, functional  
CC equivalents and/or hybrids or its mutants, and a vector comprising a  
CC polynucleotide encoding (I) are useful as agents for treating  
CC degenerative disorders including disorders having inappropriate cell  
CC proliferation or inappropriate cell death. The agents are also useful for  
CC treating disorders in which a cell is present and/or persists in an  
CC inappropriate location, and autoimmune disease such as systemic lupus  
CC erythematosus (SLE) and rheumatoid arthritis. The degenerative disorder  
CC include acquired immunodeficiency syndrome (AIDS). This is the amino acid  
CC sequence of a Bcl-2 family member GD domain peptide.

XX SQ Sequence 20 AA;  
Query Match 100.0%; Score 104; DB 8; Length 20;

Best Local Similarity 100.0%; Pred. No. 4.4e-10;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADPLHEAMRAAGDEFETRF 20  
DB 1 AADPLHEAMRAAGDEFETRF 20  
|||||

RESULT 3  
AAB37024  
ID AAB37024 standard; peptide; 27 AA.  
XX AC AAB37024;  
XX DT 28-FEB-2001 (first entry)  
XX DE Bcl2 polypeptide BH3 domain peptide #24.  
XX KW Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective;  
KW cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad;  
KW apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;  
KW colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;  
KW melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS; stroke;  
KW myocardial infarction.  
XX OS Homo sapiens.  
XX PN WO200059526-A1.  
XX PD 12-OCT-2000.  
XX PF 06-APR-2000; 2000WO-US009352.  
XX PR 07-APR-1999; 99US-0128202P.  
XX (UYJE-) UNIV JEFFERSON THOMAS.  
XX PI Huang Z, Wang J, Zhang Z, Shan S, Lu Z;  
XX WPI; 2000-679325/66.  
XX

New peptide conjugates for modulating apoptosis or for inhibiting B cell  
PT lymphoma/leukemia 2 (Bcl-2) function, especially useful for treating  
PT neurodegenerative disorders, stroke, or cancer.  
XX

Claim 18; Page 18; 74pp; English.

The invention relates to a peptide conjugate having the formula: (R-X)n-  
CC peptide where n = 1-10; X = C=O, when the R-X group is attached to the N-  
CC terminus of the peptide, or a side chain of the peptide where the  
CC functional group of the side chain is NH2 or OH; or X = O or NH, when the  
CC R-X group is attached to the C-terminus of the peptide, or a side chain  
CC of the peptide, where the side chain functional group is COOH or CONH2;  
CC and R = 2-18C alkyl or alkoxy, 2-14C alkylenyl containing one or two  
CC double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally  
CC nonsubstituted with a 1-5C straight or branched chain alkyl group,  
CC phenyl optionally monosubstituted with a 1-5C straight or branched chain  
CC alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples  
CC of the peptide portion of the conjugate. The peptides represent analogues  
CC of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of  
CC the BH3 domain of the cell death agonist Bad. The peptide conjugate is  
CC useful for modulating apoptosis in the cells of a subject, or for  
CC reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of  
CC apoptosis in cancer cells. It is also useful for inhibiting Bcl-2  
CC function. In particular, the peptide conjugate is useful for treating a  
CC subject afflicted with a cancer characterized by cancer cells that  
CC express Bcl-2. The cancer includes prostate, colorectal, gastric, non-  
CC small lung, renal or thyroid cancers, neuroblastoma, melanoma, or acute  
CC or chronic lymphocytic and non-lymphocytic leukemia. The peptide  
CC conjugate is also useful for treating disorders characterized by  
CC increased apoptosis, e.g. neurodegenerative disorders, acquired  
CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction  
XX

SQ Sequence 27' AA;

Query Match 97.1%; Score 101; DB 3; Length 27;  
Best Local Similarity 95.0%; Pred. No. 2e-09;  
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADPLHEAMRAAGDEFETRF 20  
|||||:|||||  
Db 4 AADPLHQAMRAAGDEFETRF 23

RESULT 4  
AAW36048  
ID AAW36048 standard; protein; 168 AA.

AC AAW36048;

DT 22-APR-1998 (first entry)

DE Mouse bcl-w protein.

KW Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;  
KW diagnosis; degenerative disease.

OS Mus sp.

PN W09735971-A1.

PD 02-OCT-1997.

PF 27-MAR-1997; 97WO-AU000199.

PR 27-MAR-1996; 96AU-00008965.

PA (AMRA-) AMRAD OPERATIONS PTY LTD.

PI Cory S, Adams JM, Gibson LM, Holmgreen SP;

DR WPI; 1997-489635/45.

DR N-PSDB; AAT96578.

PT Nucleic acid encoding apoptosis related gene bcl-w - used to induce or  
PT inhibit cell survival, e.g. for treatment of cancer and degenerative  
PT diseases.

PS Claim 6; Page 50-51; 86pp; English.

XX This sequence represents a novel protein, bcl-w, encoded by the mouse bcl  
CC -2 gene family. This gene promotes cell survival, so its modulation is  
CC useful in treatment of cancer or auto-immune diseases, degenerative  
CC diseases (e.g. stroke, Alzheimer's disease, myocardial infarct, muscular  
CC degeneration, hypoxia, ischaemia, human immunodeficiency virus infection  
CC or in cell transplants. Up-regulation of the gene can also be used to  
CC modify cell lines cultured in vivo, e.g. to develop new lines, to  
CC facilitate isolation of hybridomas and to increase survival of primary  
CC explants during genetic modification. It can be used to produce  
CC recombinant Bcl-w for therapy, diagnosis, antibody production or  
CC screening of potential modulators

XX Sequence 168 AA;

Query Match 97.1%; Score 101; DB 2; Length 168;  
Best Local Similarity 95.0%; Pred. No. 1.8e-08;  
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADPLHEAMRAAGDEFETRF 20  
|||||:|||||  
Db 38 AADPLHQAMRAAGDEFETRF 57

RESULT 5  
ADP88350  
ID ADP88350 standard; protein; 183 AA.

XX ADP88350;

XX 09-SEP-2004 (first entry)

XX Derivative of human Bcl-w protein.

XX Bcl-w; human; protein structure; protein co-ordinate data; mutant;  
XX mutein.

OS Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 128

FT /note= "wild-type Ala substituted by Glu"

XX W02004050697-A1.

XX 17-JUN-2004.

XX 03-DEC-2003; 2003WO-AU001624.

XX 03-DEC-2002; 2002AU-00953259.

XX (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.

XX Hinds MG, Huang DCS, Day CL;

XX WPI; 2004-487529/46.

XX Solution useful for identifying or selecting agents that are capable of  
XX inhibiting biological activity of Bcl-w, comprises molecule that has Bcl-  
XX w active site defined by specific structure coordinates of Bcl-w amino  
XX acid residues.

XX Claim 16; Page 805-806; 810pp; English.

XX The present invention relates to a solution comprising a molecule or  
CC molecular complex that comprises at least a fragment of Bcl-w. Also  
CC disclosed is the structure of Bcl-w, in the form of protein coordinate  
CC data. The solution is useful for identifying, selecting or designing  
CC agents that are capable of inhibiting or potentiating one or more  
CC biological activity of Bcl-w, and in solving the structures of other  
CC proteins with similar structure. It is also useful for characterizing the  
CC three-dimensional structure of the Bcl-w molecule, molecular complex or  
CC its derivative. The present sequence is a derivative of the human Bcl-w  
CC protein.

XX Sequence 183 AA;

Query Match 97.1%; Score 101; DB 8; Length 183;  
Best Local Similarity 95.0%; Pred. No. 2e-08;  
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADPLHEAMRAAGDEFETRF 20  
|||||:|||||  
Db 38 AADPLHQAMRAAGDEFETRF 57

RESULT 6

AAW97394

ID AAW97394 standard; protein; 192 AA.

AC AAW97394;

XX 20-MAY-1999 (first entry)

XX Mammalian bcl-y protein.

XX Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;

XX programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;  
KW head trauma; Alzheimer's Disease; neural; muscular degenerative disease;

KW multiple sclerosis; myocardial infarction; vitally induced cell death;  
 KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;  
 KW premature cell death; cell death stimulator; prolonged cell life span;  
 KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite.  
 OS Mammalia.  
 XX  
 PN US5883229-A.  
 XX  
 XX 16-MAR-1999.  
 PD  
 XX  
 XX 25-NOV-1997; 97US-00978523.  
 XX  
 XX 23-FEB-1996; 96US-0012201P.  
 PR 11-FEB-1997; 97US-00798897.  
 XX  
 XX (COCE-) COCENSYS INC.  
 PA  
 XX  
 XX Guastella J;  
 PI  
 XX  
 XX WPI; 1999-214150/18.  
 DR  
 XX  
 XX Novel bcl-y homologues of the rat and human bcl-2 protein - useful for  
 PT modulating programmed cell death.  
 PT  
 XX  
 XX Claim 2; Col 19-22; 26pp; English.  
 PS  
 XX The present sequence represents a mammalian bcl-2 protein. The  
 CC specification describes rat bcl-y protein (Rbcl-y) and human bcl-y  
 CC protein (Hbcl-y). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein  
 CC thought to be involved in programmed cell death (apoptosis and necrosis).  
 CC Rbcl-y and Hbcl-y proteins may be used to treat conditions associated  
 CC with a disruption of the cell death pathway. If they act as cell death  
 CC inhibitors, they may be used in therapies to treat subjects suffering  
 CC from: strokes, head trauma, Alzheimer's Disease, neural and muscular  
 CC degenerative diseases (especially multiple sclerosis), myocardial  
 CC infarction, vitally induced cell death, aging, spinal cord injuries and  
 CC amyotrophic lateral sclerosis- conditions where cells under go premature  
 CC cell death as a result of triggers which may or may not be apparent. They  
 CC may also be used in this way to develop cell lines which remain viable in  
 CC culture for an extended period. In contrast, if they act as cell death  
 CC stimulators, Rbcl-y and Hbcl-y may be used to treat conditions associated  
 CC with prolonged cell life span such as cancer (especially Kaposi's sarcoma  
 CC and lung cancer) and auto/hyperimmune diseases. They may also be used to  
 CC cause cell death in, and hence control, parasites  
 CC  
 XX Sequence 192 AA;  
 SQ  
 Query Match 97.1%; Score 101; DB 2; Length 192;  
 Best Local Similarity 95.0%; Pred. No. 2.1e-08;  
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AADPLHEAMRAAGDEFETRF 20  
 Db |||||:|||||  
 37 AADPLHQAMRAAGDEFETRF 56  
 RESULT 7  
 AAW97393  
 ID AAW97393 standard; protein; 192 AA.  
 XX  
 XX AAW97393;  
 AC  
 XX 20-MAY-1999 (first entry)  
 DT  
 XX Protein sequence of the specification.  
 DE  
 XX Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;  
 KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;  
 KW head trauma; Alzheimer's Disease; neural; muscular degenerative disease;  
 KW multiple sclerosis; myocardial infarction; vitally induced cell death;  
 KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;  
 KW premature cell death; cell death stimulator; prolonged cell life span;

KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite.  
 XX Unidentified.  
 OS  
 XX US5883229-A.  
 PN  
 XX 16-MAR-1999.  
 PD  
 XX  
 XX 25-NOV-1997; 97US-00978523.  
 XX  
 XX 23-FEB-1996; 96US-0012201P.  
 PR 11-FEB-1997; 97US-00798897.  
 XX  
 XX (COCE-) COCENSYS INC.  
 PA  
 XX  
 XX Guastella J;  
 PI  
 XX  
 XX WPI; 1999-214150/18.  
 DR  
 XX  
 XX Novel bcl-y homologues of the rat and human bcl-2 protein - useful for  
 PT modulating programmed cell death.  
 PT  
 XX  
 XX Disclosure; Col 19-20; 26pp; English.  
 PS  
 XX The specification describes rat bcl-y protein (Rbcl-y) and human bcl-y  
 CC protein (Hbcl-y). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein  
 CC thought to be involved in programmed cell death (apoptosis and necrosis).  
 CC Rbcl-y and Hbcl-y proteins may be used to treat conditions associated  
 CC with a disruption of the cell death pathway. If they act as cell death  
 CC inhibitors, they may be used in therapies to treat subjects suffering  
 CC from: strokes, head trauma, Alzheimer's Disease, neural and muscular  
 CC degenerative diseases (especially multiple sclerosis), myocardial  
 CC infarction, vitally induced cell death, aging, spinal cord injuries and  
 CC amyotrophic lateral sclerosis- conditions where cells under go premature  
 CC cell death as a result of triggers which may or may not be apparent. They  
 CC may also be used in this way to develop cell lines which remain viable in  
 CC culture for an extended period. In contrast, if they act as cell death  
 CC stimulators, Rbcl-y and Hbcl-y may be used to treat conditions associated  
 CC with prolonged cell life span such as cancer (especially Kaposi's sarcoma  
 CC and lung cancer) and auto/hyperimmune diseases. They may also be used to  
 CC cause cell death in, and hence control, parasites  
 CC  
 XX Sequence 192 AA;  
 SQ  
 Query Match 97.1%; Score 101; DB 2; Length 192;  
 Best Local Similarity 95.0%; Pred. No. 2.1e-08;  
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AADPLHEAMRAAGDEFETRF 20  
 Db |||||:|||||  
 37 AADPLHQAMRAAGDEFETRF 56  
 RESULT 8  
 AAY05533  
 ID AAY05533 standard; protein; 192 AA.  
 XX  
 XX AAY05533;  
 AC  
 XX 05-JUL-1999 (first entry)  
 DT  
 XX Mouse Bcl-w protein derivative.  
 DE  
 XX Spermatogenesis; Bcl-3; Bcl-2; mouse; fertility; infertility;  
 KW animal model.  
 KW  
 XX Mus sp.  
 OS  
 XX WO9913710-A1.  
 PN  
 XX 25-MAR-1999.  
 PD  
 XX 16-SEP-1998; 98WO-AU000764.  
 PF



XX 16-SEP-1997; 97AU-00009228.  
 XX (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.  
 XX Cory S, Adams J, Print C, Gibson L, Koentgen F;  
 XX WPI; 1999-243890/20.  
 XX N-PSDB; AAX251135.  
 XX An animal model exhibiting reduced levels of a Bcl-w protein and/or  
 XX protein associated with Bcl-w.  
 XX Disclosure; Page 39; 52pp; English.  
 XX The present sequence is described of a derivative of mouse Bcl-w (see  
 CC also AAY05531) a pro-survival member of the Bcl-2 family that is widely  
 CC expressed and which is essential for spermatogenesis. The derivative  
 CC lacks the 24 N-terminal amino acids of Bcl-w. The invention relates  
 CC generally to a method of treatment and to an animal model for the  
 CC identification of molecules and genetic sequences useful for inducing or  
 CC reducing fertility of male animals. Methods are provided for the  
 CC treatment of infertility, or for reducing fertility, by modulating  
 CC spermatogenesis. An animal model carries a mutation is at least one  
 CC allele of the human or murine bcl-w gene (see AAX25132-35) or in a gene  
 CC associated with bcl-w. Such animals have disorganised seminiferous tubules  
 CC and are substantially infertile, but possess no other major abnormalities  
 CC as determined by histological examination. They can be used to screen for  
 CC therapeutic molecules including genetic sequences capable of inducing,  
 CC enhancing or otherwise facilitating spermatogenesis in animals, or which  
 CC can induce infertility  
 XX  
 XX Sequence 192 AA;  
 SQ

Query Match 97.1%; Score 101; DB 2; Length 192;  
 Best Local Similarity 95.0%; Pred. No. 2.1e-08;  
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADPLHEAMRAAGDEFETRF 20  
 |||||:|||||  
 Db 38 AADPLHQAMRAAGDEFETRF 57

RESULT 9  
 AAW36047  
 ID AAW36047 standard; protein; 193 AA.  
 XX  
 AC AAW36047;  
 XX  
 DT 22-APR-1998 (first entry)  
 XX  
 DE Human bcl-w protein.  
 XX  
 KW Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;  
 XX diagnosis; degenerative disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9735971-A1.  
 XX  
 PD 02-OCT-1997.  
 XX  
 PF 27-MAR-1997; 97WO-AU000199.  
 XX  
 PR 27-MAR-1996; 96AU-00008965.  
 XX  
 PA (AMRA-) AMRAD OPERATIONS PTY LTD.  
 XX  
 PI Cory S, Adams JM, Gibson LM, Holmgren SP;  
 XX WPI; 1997-489635/45.  
 XX N-PSDB; AAT96577.  
 XX

PT Nucleic acid encoding apoptosis related gene bcl-w - used to induce or  
 PT inhibit cell survival, e.g. for treatment of cancer and degenerative  
 XX diseases.  
 XX  
 XX Claim 6; Page 48; 86pp; English.  
 XX  
 CC This sequence represents a novel human protein, bcl-w, encoded by the bcl  
 CC -2 gene family and extracted from an adult brain library. This gene  
 CC promotes cell survival, so its modulation is useful in treatment of  
 CC cancer or auto-immune diseases, degenerative diseases (e.g. stroke,  
 CC Alzheimer's disease, myocardial infarct, muscular degeneration, hypoxia,  
 CC ischaemia, human immunodeficiency virus infection or in cell transplants.  
 CC Up-regulation of the gene can also be used to modify cell lines cultured  
 CC in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas  
 CC and to increase survival of primary explants during genetic modification.  
 CC It can be used to produce recombinant Bcl-w for therapy, diagnosis,  
 CC antibody production or screening of potential modulators  
 XX  
 XX Sequence 193 AA;  
 SQ

Query Match 97.1%; Score 101; DB 2; Length 193;  
 Best Local Similarity 95.0%; Pred. No. 2.1e-08;  
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADPLHEAMRAAGDEFETRF 20  
 |||||:|||||  
 Db 38 AADPLHQAMRAAGDEFETRF 57

RESULT 10  
 AAW61392  
 ID AAW61392 standard; protein; 193 AA.  
 XX  
 AC AAW61392;  
 XX  
 DT 02-OCT-1998 (first entry)  
 XX  
 DE Human bcl-y protein.  
 XX  
 KW bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US5789201-A.  
 XX  
 PD 04-AUG-1998.  
 XX  
 PF 11-FEB-1997; 97US-00798897.  
 XX  
 PR 23-FEB-1996; 96US-0012201P.  
 XX  
 PA (COCE-) COCENSYS INC.  
 XX  
 XX Guastella J;  
 PI  
 XX WPI; 1998-446079/38.  
 XX  
 DR N-PSDB; AAV28334.  
 XX  
 PT Nucleic acids encoding B-cell lymphoma-y protein - useful for producing  
 PT recombinant protein for use in treating uncontrolled cell growth e.g.  
 PT cancers.  
 XX  
 XX Example; Column 17/18; 27pp; English.  
 XX  
 CC The mammalian bcl-y protein is a member of the bcl-2 family, components  
 CC in the cell death pathway. The bcl-2 family have both apoptotic activity  
 CC and the apoptosis blocking activity. bcl-y falls in the apoptosis  
 CC activity category. The recombinant protein may be used to prevent  
 CC uncontrolled cell growth, either by its direct administration to  
 CC recombinant genetic constructs to increase its expression in vivo. Also,  
 CC antisense constructs can be used in disorders where prevention of cell  
 CC death is desired  
 XX

```

SQ Sequence 193 AA;
  Query Match          97.1%; Score 101; DB 2; Length 193;
  Best Local Similarity 95.0%; Pred. No. 2.1e-08;
  Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADPLHEAMRAAGDEFETRF 20
    |||||:|||||
Db 38 AADPLHQAMRAAGDEFETRF 57

RESULT 11
AAW61391
ID AAW61391 standard; protein; 193 AA.
XX
AC AAW61391;
XX
DT 02-OCT-1998 (first entry)
XX
DE Rat bcl-y protein.
XX
KW bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; rat.
XX
OS Rattus sp.
XX
PN US5789201-A.
XX
PD 04-AUG-1998.
XX
PF 11-FEB-1997; 97US-00798897.
XX
PR 23-FEB-1996; 96US-0012201P.
XX
PA (COCE-) COCENSYS INC.
XX
PI Guastella J;
XX
WPI; 1998-446079/38.
DR N-PSDB; AAV28333.
XX
XX Nucleic acids encoding B-cell lymphoma-y protein - useful for producing
PT recombinant protein for use in treating uncontrolled cell growth e.g.
PT cancers.
XX
PS Example; Fig 3A; 27pp; English.
XX
CC The mammalian bcl-y protein is a member of the bcl-2 family, components
CC in the cell death pathway. The bcl-2 family have both apoptotic activity
CC and the apoptosis blocking activity. bcl-y falls in the apoptosis
CC activity category. The recombinant protein may be used to prevent
CC uncontrolled cell growth, either by its direct administration to
CC recombinant genetic constructs to increase its expression in vivo. Also,
CC antisense constructs can be used in disorders where prevention of cell
CC death is desired
XX
SQ Sequence 193 AA;
  Query Match          97.1%; Score 101; DB 2; Length 193;
  Best Local Similarity 95.0%; Pred. No. 2.1e-08;
  Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADPLHEAMRAAGDEFETRF 20
    |||||:|||||
Db 38 AADPLHQAMRAAGDEFETRF 57

RESULT 12
AAW97392
ID AAW97392 standard; protein; 193 AA.
XX
AC AAW97392;
XX
DT 20-MAY-1999 (first entry)
XX
DE The rat bcl-y protein.

XX
DE The human bcl-y protein.
XX
KW Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;
KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
KW head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
KW multiple sclerosis; myocardial infarction; vitally induced cell death;
KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
KW premature cell death; cell death stimulator; prolonged cell life span;
KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite.
XX
OS Homo sapiens.
XX
PN US5883229-A.
XX
PD 16-MAR-1999.
XX
PF 25-NOV-1997; 97US-00978523.
XX
PR 23-FEB-1996; 96US-0012201P.
PR 11-FEB-1997; 97US-00798897.
XX
PA (COCE-) COCENSYS INC.
XX
PI Guastella J;
XX
WPI; 1999-214150/18.
DR N-PSDB; AAX15946.
XX
PT Novel bcl-y homologues of the rat and human bcl-2 protein - useful for
PT modulating programmed cell death.
XX
PS Claim 1; Col 17-18; 26pp; English.
XX
CC The present sequence represents human bcl-y protein (Hbcl-y). The
CC specification also describes rat bcl-y protein (Rbcl-y). Rbcl-y and Hbcl-
CC y are homologues of the bcl-2 protein thought to be involved in
CC programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y
CC proteins may be used to treat conditions associated with a disruption of
CC the cell death pathway. If they act as cell death inhibitors, they may be
CC used in therapies to treat subjects suffering from: strokes, head trauma,
CC Alzheimer's Disease, neural and muscular degenerative diseases
CC (especially multiple sclerosis), myocardial infarction, vitally induced
CC cell death, aging, spinal cord injuries and amyotrophic lateral sclerosis
CC - conditions where cells under go premature cell death as a result of
CC triggers which may or may not be apparent. They may also be used in this
CC way to develop cell lines which remain viable in culture for an extended
CC period. In contrast, if they act as cell death stimulators, Rbcl-y and
CC Hbcl-y may be used to treat conditions associated with prolonged cell
CC life span such as cancer (especially Kaposi's sarcoma and lung cancer)
CC and auto/hyperimmune diseases. They may also be used to cause cell death
CC in, and hence control, parasites
XX
SQ Sequence 193 AA;
  Query Match          97.1%; Score 101; DB 2; Length 193;
  Best Local Similarity 95.0%; Pred. No. 2.1e-08;
  Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADPLHEAMRAAGDEFETRF 20
    |||||:|||||
Db 38 AADPLHQAMRAAGDEFETRF 57

RESULT 13
AAW97391
ID AAW97391 standard; protein; 193 AA.
XX
AC AAW97391;
XX
DT 20-MAY-1999 (first entry)
XX
DE The rat bcl-y protein.

```

XX Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;  
 KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;  
 KW head trauma; Alzheimer's disease; neural; muscular degenerative disease;  
 KW multiple sclerosis; myocardial infarction; vitally induced cell death;  
 KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;  
 KW premature cell death; cell death stimulator; prolonged cell life span;  
 KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite.  
 XX Rattus sp.  
 XX OS  
 XX US5883229-A.  
 XX PN  
 XX 16-MAR-1999.  
 XX PD  
 XX 25-NOV-1997; 97US-00978523.  
 XX PF  
 XX 23-FEB-1996; 96US-0012201P.  
 XX PR  
 XX 11-FEB-1997; 97US-00798897.  
 XX PR  
 XX (COCE-) COCENSYS INC.  
 XX PA  
 XX Guastella J;  
 XX PI  
 XX WPI; 1999-214150/18.  
 XX DR  
 XX N-PSDB; AAX15945.  
 XX DR  
 XX Novel bcl-y homologues of the rat and human bcl-2 protein - useful for  
 PT modulating programmed cell death.  
 XX PT  
 XX Disclosure; Col 15-18; 26pp; English.  
 XX PS  
 XX The present sequence represents rat bcl-y protein (Rbcl-y). The  
 CC specification also describes human bcl-y protein (Hbcl-y). Rbcl-y and  
 CC Hbcl-y are homologues of the bcl-2 protein thought to be involved in  
 CC programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y  
 CC proteins may be used to treat conditions associated with a disruption of  
 CC the cell death pathway. If they act as cell death inhibitors, they may be  
 CC used in therapies to treat subjects suffering from: strokes, head trauma,  
 CC Alzheimer's Disease, neural and muscular degenerative diseases  
 CC (especially multiple sclerosis), myocardial infarction, vitally induced  
 CC cell death, aging, spinal cord injuries and amyotrophic lateral sclerosis  
 CC - conditions where cells under go premature cell death as a result of  
 CC triggers which may or may not be apparent. They may also be used in this  
 CC way to develop cell lines which remain viable in culture for an extended  
 CC period. In contrast, if they act as cell death stimulators, Rbcl-y and  
 CC Hbcl-y may be used to treat conditions associated with prolonged cell  
 CC life span such as cancer (especially Kaposi's sarcoma and lung cancer)  
 CC and auto/hyperimmune diseases. They may also be used to cause cell death  
 CC in, and hence control, parasites  
 XX in, and hence control, parasites  
 XX SQ  
 XX Sequence 193 AA;  
 Query Match 97.1%; Score 101; DB 2; Length 193;  
 Best Local Similarity 95.0%; Pred. No. 2.1e-08;  
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AADPLHEAMRAAGDEPETF 20  
 DB 38 AADPLHQAMRAAGDEPETF 57  
 RESULT 14  
 AAY05530  
 ID AAY05530 standard; protein; 193 AA.  
 XX AC  
 XX AAY05530;  
 XX DT  
 XX 05-JUL-1999 (first entry)  
 XX DE  
 XX Human Bcl-w protein essential for spermatogenesis.  
 XX KW  
 XX Spermatogenesis; Bcl-3; Bcl-2; human; fertility; infertility;  
 XX animal model.  
 XX OS  
 XX Homo sapiens.  
 XX PN  
 XX WO9913710-A1.  
 XX PD  
 XX 25-MAR-1999.  
 XX PF  
 XX 16-SEP-1998; 98WO-AU000764.  
 XX PR  
 XX 16-SEP-1997; 97AU-00009228.  
 XX PR  
 XX Spermatogenesis; Bcl-3; Bcl-2; human; fertility; infertility;  
 XX animal model.  
 XX OS  
 XX Homo sapiens.  
 XX PN  
 XX WO9913710-A1.  
 XX PD  
 XX 25-MAR-1999.  
 XX PF  
 XX 16-SEP-1998; 98WO-AU000764.  
 XX PR  
 XX 16-SEP-1997; 97AU-00009228.  
 XX PR

KW animal model.  
 XX OS  
 XX Homo sapiens.  
 XX PN  
 XX WO9913710-A1.  
 XX PD  
 XX 25-MAR-1999.  
 XX PF  
 XX 16-SEP-1998; 98WO-AU000764.  
 XX PR  
 XX 16-SEP-1997; 97AU-00009228.  
 XX PR  
 XX (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.  
 XX PA  
 XX Cory S, Adams J, Print C, Gibson L, Koentgen F;  
 XX WPI; 1999-243890/20.  
 XX DR  
 XX N-PSDB; AAX25132.  
 XX DR  
 XX An animal model exhibiting reduced levels of a Bcl-w protein and/or  
 PT protein associated with Bcl-w.  
 XX PT  
 XX Claim 2; Page 33; 52pp; English.  
 XX PS  
 XX The present sequence is human Bcl-w, a pro-survival member of the Bcl-2  
 CC family which is widely expressed and which is essential for  
 CC spermatogenesis. The invention relates generally to a method of treatment  
 CC and to an animal model for the identification of molecules and genetic  
 CC sequences useful for inducing or reducing fertility of male animals.  
 CC Methods are provided for the treatment of infertility, or for reducing  
 CC fertility, by modulating spermatogenesis. An animal model carries a  
 CC mutation is at least one allele of the human or murine bcl-w gene (see  
 CC AAX25132-35) or in a gene associated with bcl-w. Such animals have  
 CC disorganised seminiferous tubules and are substantially infertile, but  
 CC possess no other major abnormalities as determined by histological  
 CC examination. They can be used to screen for therapeutic molecules  
 CC including genetic sequences capable of inducing, enhancing or otherwise  
 CC facilitating spermatogenesis in animals, or which can induce infertility  
 XX in, and hence control, parasites  
 XX SQ  
 XX Sequence 193 AA;  
 Query Match 97.1%; Score 101; DB 2; Length 193;  
 Best Local Similarity 95.0%; Pred. No. 2.1e-08;  
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AADPLHEAMRAAGDEPETF 20  
 DB 38 AADPLHQAMRAAGDEPETF 57  
 RESULT 15  
 AAY05532  
 ID AAY05532 standard; protein; 193 AA.  
 XX AC  
 XX AAY05532;  
 XX DT  
 XX 05-JUL-1999 (first entry)  
 XX DE  
 XX Human Bcl-w protein essential for spermatogenesis.  
 XX KW  
 XX Spermatogenesis; Bcl-3; Bcl-2; human; fertility; infertility;  
 XX animal model.  
 XX OS  
 XX Homo sapiens.  
 XX PN  
 XX WO9913710-A1.  
 XX PD  
 XX 25-MAR-1999.  
 XX PF  
 XX 16-SEP-1998; 98WO-AU000764.  
 XX PR  
 XX 16-SEP-1997; 97AU-00009228.  
 XX PR

PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.  
XX  
PI Cory S, Adams J, Print C, Gibson L, Koentgen F;  
XX  
DR WPI; 1999-243890/20.  
DR N-PSDB; AAX25134.  
XX  
PT An animal model exhibiting reduced levels of a Bcl-w protein and/or  
PT protein associated with Bcl-w.  
XX  
PS Disclosure; Page 37; 52pp; English.  
XX  
XX The present sequence is described of a derivative of human Bcl-w (see  
CC also AAY05530), a pro-survival member of the Bcl-2 family that is widely  
CC expressed and which is essential for spermatogenesis. The invention  
CC relates generally to a method of treatment and to an animal model for the  
CC identification of molecules and genetic sequences useful for inducing or  
CC reducing fertility of male animals. Methods are provided for the  
CC treatment of infertility, or for reducing fertility, by modulating  
CC spermatogenesis. An animal model carries a mutation, is at least one  
CC allele of the human or murine bcl-w gene (see AAX25132-35) or in a gene  
CC associated with bcl-w. Such animals have disorganised seminiferous tubules  
CC and are substantially infertile, but possess no other major abnormalities  
CC as determined by histological examination. They can be used to screen for  
CC therapeutic molecules including genetic sequences capable of inducing,  
CC enhancing or otherwise facilitating spermatogenesis in animals, or which  
CC can induce infertility  
XX  
SQ Sequence 193.AA;

Query Match 97.1%; Score 101; DB 2; Length 193;  
Best Local Similarity 95.0%; Pred. No. 2.1e-08;  
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADPLHEAMRAGDEFETRF 20  
|||||:|||||  
DB 38 AADPLHQMAMRAGDEFETRF 57

Search completed: January 25, 2005, 10:14:37  
Job time : 119.5 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 25, 2005, 10:06:01 ; Search time 132 Seconds  
(without alignments)  
87.178 Million cell updates/sec

Title: US-09-828-870-39

Perfect score: 104

Sequence: 1 AADPLHEAMRAAGDEFETRF 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt\_02:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	101	97.1	178	Q8CFR2	Q8cfw2 mus musculus
2	101	97.1	178	Q9CYW5	Q9cyw5 mus musculus
3	101	97.1	193	1 BCLW HUMAN	Q92843 homo sapien
4	101	97.1	193	1 BCLW MOUSE	P70345 mus musculus
5	101	97.1	193	2 O88996	O88996 rattus norv
6	101	97.1	193	2 BAB23468	Bab23468 mus muscu
7	101	97.1	219	2 Q7TS60	Q7ts60 rattus norv
8	92	88.5	193	2 O8CG14	O8cg14 mus musculus
9	73	70.2	188	2 O6GP82	O6gp82 xenopus lae
10	73	70.2	228	1 ARL1 XENLA	Q91827 xenopus lae
11	54	51.9	89	2 Q8UWU1	Q8uwj1 gallus gall
12	54	51.9	229	1 BCLX CHICK	Q07816 gallus gall
13	51	49.0	125	2 Q9H1R5	Q9h1r5 homo sapien
14	51	49.0	170	2 Q9WU15	Q9wu15 rattus norv
15	51	49.0	170	2 AAF81262	Aaf81262 rattus no
16	51	49.0	180	2 Q9BDD5	Q9bdd5 bos taurus
17	51	49.0	180	2 Q9BDX7	Q9bdx7 bos taurus
18	51	49.0	188	2 Q9H1R6	Q9h1r6 homo sapien
19	51	49.0	188	2 Q9QWX2	Q9qwx2 mus musculus
20	51	49.0	217	2 Q99N35	Q99n35 mus musculus
21	51	49.0	219	2 Q99N36	Q99n36 mus musculus
22	51	49.0	233	1 BCLX HUMAN	Q07817 homo sapien
23	51	49.0	233	1 BCLX MOUSE	Q64373 mus musculus
24	51	49.0	233	1 BCLX PIG	Q07737 sus scrofa
25	51	49.0	233	1 BCLX RAT	P53563 rattus norv
26	51	49.0	233	2 Q61L77	Q61l77 canis fami
27	51	49.0	233	2 Q9MYW4	Q9myw4 oryctolagus
28	51	49.0	233	2 Q9MZ57	Q9mz57 ovis aries
29	51	49.0	233	2 Q9N1A2	Q9n1a2 sus scrofa
30	51	49.0	233	2 Q8SQ42	Q8sq42 felis silve
31	51	49.0	233	2 BAB71819	Bab71819 canis fam

#### RESULT 1

ID	Q8CFR2	PRELIMINARY;	PRT;	178 AA.
AC	Q8CFR2;			
DT	01-MAR-2003 (Tremblrel. 23, Created)			
DT	01-MAR-2003 (Tremblrel. 23, Last sequence update)			
DT	01-OCT-2003 (Tremblrel. 25, Last annotation update)			
DE	Bcl2l2 protein.			
GN	Name=Bcl2l2;			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Eye;			
RC	MEDLINE=22388257; PubMed=12477932;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh P., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., White J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalek U., Smalish D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Eye;			
RC	Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.			
RA	EMBL; BC040369; AAH40369.1; -			
DR	HSSP; Q92843; 100L			
DR	MGP; MGI:108052; Bcl2l2.			
DR	GO; GO:0005515; P:protein binding; IPI.			
DR	GO; GO:0006915; P:apoptosis; IDA.			
DR	InterPro; IPR000712; Bcl2_BH.			
DR	InterPro; IPR003093; Bcl2_BH4.			
DR	InterPro; IPR002475; BCL2_family.			
DR	Pfam; PF00452; Bcl-2; 1.			
DR	Pfam; PF02180; BH4; 1.			
DR	SMART; SM00337; BCL; 1.			
DR	SMART; SM00265; BH4; 1.			

#### ALIGNMENTS

32	51	49.0	233	2	AAP35872
33	51	49.0	235	2	O35843
34	51	49.0	284	2	Q7TS62
35	50	48.1	233	1	BCL2 CHICK
36	49	47.1	610	2	Q91781
37	48	46.2	179	2	Q6VWH2
38	48	46.2	179	2	BAD16383
39	48	46.2	325	2	Q73W86
40	48	46.2	325	2	AAS05091
41	48	46.2	942	2	O82EJ4
42	48	46.2	952	1	TOPI STRCO
43	48	46.2	1788	2	Q81G61
44	47	45.2	186	2	Q9FYK2
45	47	45.2	392	2	Q6D7P3

Aap35872 homo sapi  
O35843 mus musculus  
Q7ts62 rattus norv  
Q00709 gallus gall  
Q91781 pseudomonas  
Q6ywh2 oryza sativ  
Bad16383 oryza sat  
Q73w86 mycobacteri  
Aas05091 mycobacte  
O82ej4 streptomyce  
Q9x909 streptomyce  
Q81g61 caenorhabdi  
Q9fyk2 arabidopsie  
Q6d7p3 erwinia car

```

DR PROSITE; PS50062; BCL2 FAMILY; 1.
DR PROSITE; PS01080; BH1_1; 1.
DR PROSITE; PS01260; BH4_1; 1.
DR PROSITE; PS50063; BH4_2; 1.
SQ SEQUENCE 178 AA; 19119 MW; E2C3F3F79528E9D7 CRC64;

Query Match 97.1%; Score 101; DB 2; Length 178;
Best Local Similarity 95.0%; Pred. No. 1.5e-07;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADPLHEAMRAAGDEFETRF 20
    |||||:|||||
Db 38 AADPLHQAMRAAGDEFETRF 57
    |||||:|||||

RESULT 2
Q9CYW5 PRELIMINARY; PRT; 178 AA.
AC Q9CYW5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Mus musculus 10, 11 days embryo whole body cDNA, RIKEN full-length
DE enriched library, clone:2810435a13 product:Bcl2-like 2, full insert
DE sequence.
GN Name=Bcl2l2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RA The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=2049374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Osawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format

```

```

RT sequencing pipeline with 384 multicapillary sequencer.";
RN Genome Res. 10:1757-1771(2000).
RP [6]
SQ SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai T.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK013244; BAB28740.1; -.
DR HSSP; Q92843; 100L;
DR MGD; MGI:108052; Bcl2l2.
DR GO; GO:0005515; P:protein binding; IPI.
DR GO; GO:0008915; P:apoptosis; IDA.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR003093; Bcl2_BH4.
DR InterPro; IPR002475; Bcl2_family.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; BH4; 1.
DR PROSITE; PS50062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01260; BH4_1; 1.
DR PROSITE; PS50063; BH4_2; 1.
SQ SEQUENCE 178 AA; 19147 MW; E2D4C3F79528E9D7 CRC64;

Query Match 97.1%; Score 101; DB 2; Length 178;
Best Local Similarity 95.0%; Pred. No. 1.5e-07;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AADPLHEAMRAAGDEFETRF 20
    |||||:|||||
Db 38 AADPLHQAMRAAGDEFETRF 57
    |||||:|||||

RESULT 3
BCLW_HUMAN STANDARD; PRT; 193 AA.
AC Q92843;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Apoptosis regulator Bcl-W (Bcl-2-like 2 protein).
GN Name=BCL2L2; Synonyms=BCLW, KIAA0271;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=96358615; PubMed=8761287;
RX Gibson L., Holmgren S.P., Huang D.C., Bernard O., Copeland N.G.,
RA Jenkins N.A., Sutherland G.R., Baker E., Adams J.M., Cory S.;
RT "bcl-w, a novel member of the bcl-2 family, promotes cell survival.";
RN [2]
RP SEQUENCE FROM N.A.
RC MEDLINE=97191544; PubMed=9039502;
RX Nagase T., Seki N., Ishikawa K.-I., Ohira M., Kawarabayashi Y.,
RA Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.;
RT "Prediction of the coding sequences of unidentified human genes. VI.
The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by
RT analysis of cDNA clones from cell line KG-1 and brain.";

```

RL DNA Res. 3:321-329(1996).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshitoki S., Carninci P., Prange C.,  
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullah S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Pahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -!- FUNCTION: Promotes cell survival.  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -!- TISSUE SPECIFICITY: Expressed in almost all myeloid cell lines and  
 in a wide range of tissues, with highest levels in brain, colon,  
 and salivary gland.  
 CC -!- DOMAIN: BH4 domain seems to be involved in the anti-apoptotic  
 function.  
 CC -!- SIMILARITY: Belongs to the Bcl-2 family.  
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.  
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.  
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use by non-profit institutions as long as its content is in no way  
 modified and this statement is not removed. Usage by and for commercial  
 entities requires a license agreement (see <http://www.isb-sib.ch/announce/>  
 or send an email to [license@sb-sib.ch](mailto:license@sb-sib.ch)).  
 CC -----  
 DR EMBL; U59747; AB03055.1; -;  
 DR EMBL; D87461; BA019666.2; ALT\_INIT.  
 DR EMBL; BC021198; AA021198.1; -;  
 DR PDB; 1MK3; NMR; A=2-172.  
 DR PDB; 1OOL; NMR; A=1-183.  
 DR Genew; HGNC:995; BCL2L2.  
 DR MIM; 601931; -;  
 DR GO; GO:0005737; Cytoplasm; NAS.  
 DR GO; GO:0006916; P:anti-apoptosis; TAS.  
 DR GO; GO:0007283; P:spermatogenesis; TAS.  
 DR InterPro; IPR007112; Bcl2 BH.  
 DR InterPro; IPR003093; Bcl2 BH4.  
 DR InterPro; IPR002475; BCL2\_family.  
 DR Pfam; PF00452; Bcl-2; 1.  
 DR Pfam; PF02180; BH4; 1.  
 DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE; PS01080; BH1; 1.  
 DR PROSITE; PS01258; BH2; 1.  
 DR PROSITE; PS01260; BH4; 1; 1.  
 DR PROSITE; PS50063; BH4; 2; 1.  
 DR 3D-structure; Apoptosis.  
 DR KW DOMAIN 9 29 BH4.  
 DR FT DOMAIN 85 104 BH1.  
 DR FT DOMAIN 136 151 BH2.  
 DR SEQUENCE 193 AA; 20774 MW; 3792243A50281761 CRC64;  
 Query Match 97.1%; Score 101; DB 1; Length 193;  
 Best Local Similarity 95.0%; Pred. No. 1.7e-07;

Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 AADPLHEAMRAAGDEFETRF 20  
 Db 38 AADPLHQAMRAAGDEFETRF 57  
 RESULT 4  
 BCLW MOUSE  
 ID BCLW MOUSE STANDARD; PRT; 193 AA.  
 AC P70345;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Apoptosis regulator Bcl-W (Bcl-2-like 2 protein).  
 GN Name=Bcl2l2; Synonyms=Bclw;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96358615; PubMed=8761287;  
 RA Gibbons L., Holmgren S.P., Huang D.C., Bernard O., Copeland N.G.,  
 RA Jenkins N.A., Sutherland G.R., Baker E., Adams J.M., Cory S.;  
 RT "bcl-w, a novel member of the bcl-2 family, promotes cell survival.";  
 RL Oncogene 13:665-675(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=C57BL/10J;  
 RA Ross A.J., Waymire K.G., Moss J.E., Parlow A.F., Skinner M.K.,  
 RA Russell L.D., Macgregor G.R.;  
 RT "Testicular degeneration in Bclw-deficient mice.";  
 RL Nat. Genet. 18:251-256(1998).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=C57BL/6J; TISSUE=Testis;  
 RC MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
 RA Nikiado I., Osato N., Sato R., Suzuki H., Yamanaka I., Kiyosawa H.,  
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,  
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Fraser K.S.,  
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,  
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
 RA Ravasi T., Reed J.C., Reid D.J., Reid J., Ring B.Z., Ringwald M.,  
 RA Sadelin A., Schneider C., Semple C.A., Setou M., Shimada K.,  
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
 RA Birney E., Hayashizaki Y.;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 60,770 full-length cDNAs.";  
 RL Nature 420:563-573(2002).  
 CC -!- FUNCTION: Promotes cell survival.  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -!- TISSUE SPECIFICITY: Expressed in almost all myeloid cell lines and  
 in a wide range of tissues, with highest levels in brain, colon,  
 and salivary gland.  
 CC

CC -1- DOMAIN: BH4 domain seems to be involved in the anti-apoptotic function.

CC -1- SIMILARITY: Belongs to the Bcl-2 family.

CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.

CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.

CC -1- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.

CC -----

CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----

CC EMBL; U59746; AAB09056.1; --

CC EMBL; AF030769; AAB86430.1; --

CC EMBL; AK015644; BAB29912.1; --

CC HSP; Q92843; 100L

CC MGD; MG1108052; Bcl1212.

CC GO; GO:000515; F:protein binding; IPI.

CC GO; GO:0006915; P:apoptosis; IDA.

CC InterPro; IPR000712; Bcl2\_BH.

CC InterPro; IPR003093; Bcl2\_BH4.

CC InterPro; IPR002475; BCL2\_family.

CC Pfam; PF00452; Bcl-2; 1.

CC Pfam; PF02180; BH4; 1.

CC PROSITE; PS00062; BCL2\_FAMILY; 1.

CC PROSITE; PS01080; BH1; 1.

CC PROSITE; PS01258; BH2; 1.

CC PROSITE; PS01260; BH4\_1; 1.

CC PROSITE; PS00063; BH4\_2; 1.

CC Apoptosis.

CC DOMAIN 9 29 BH4.

CC DOMAIN 85 104 BH1.

CC DOMAIN 136 151 BH2.

CC SEQUENCE 193 AA; 20790 MW; 36CA185F5945DFB4 CRC64;

Query Match. 97.1%; Score 101; DB 1; Length 193;  
 Best Local Similarity 95.0%; Pred. No. 1.7e-07;  
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 AADPLHEAMRAAGDEFETRF 20  
 |||||:|||||:|||||  
 38 AADPLHQAMRAAGDEFETRF 57

Db

RESULT 5

O88996 PRELIMINARY; PRT; 193 AA.

AC O88996;

DT 01-NOV-1998 (TrEMBLrel. 08, Created)

DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)

DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)

DE Bcl-w (Hypothetical protein).

GN Name=bcl-w;

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI\_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Sprague-Dawley; TISSUE=Brain;

RX MEDLINE=99292146; PubMed=10366024;

RA Hamner S., Skoglosa Y., Lindholm D.,

RT "Differential expression of bcl-w and bcl-x messenger RNA in the developing and adult rat nervous system.";

RL Neuroscience 91:673-684(1999).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=Sprague-Dawley;

RX MEDLINE=22672518; PubMed=12787069;

RA Itoh T., Itoh A., Pleasure D.;

RT "Bcl-2-related protein family gene expression during oligodendroglial differentiation.";

RT J. Neurochem. 85:1500-1512(2003).

RL [3]

RP SEQUENCE FROM N.A.

RC TISSUE=Heart;

RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smalios D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RL [4]

RP SEQUENCE FROM N.A.

RC TISSUE=Heart;

RX Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

RL EMBL; AF096291; AAC64200.1; --

DR EMBL; AY185098; AAO64468.1; --

DR EMBL; BC074021; AAH74021.1; --

DR HSP; Q92843; 100L.

DR GO; GO:0042981; P:regulation of apoptosis; IEA.

DR InterPro; IPR007112; Bcl2\_BH.

DR InterPro; IPR003093; Bcl2\_BH4.

DR InterPro; IPR002475; BCL2\_family.

DR Pfam; PF00452; Bcl-2; 1.

DR Pfam; PF02180; BH4; 1.

DR SMART; SM00337; BCL; 1.

DR SMART; SM00265; BH4; 1.

DR PROSITE; PS00062; BCL2\_FAMILY; 1.

DR PROSITE; PS01080; BH1; 1.

DR PROSITE; PS01258; BH2; 1.

DR PROSITE; PS01260; BH4\_1; 1.

DR PROSITE; PS00063; BH4\_2; 1.

KW Hypothetical protein.

'SQ SEQUENCE 193 AA; 20820 MW; 36D6742F4529AFB4 CRC64;

Query Match. 97.1%; Score 101; DB 2; Length 193;  
 Best Local Similarity 95.0%; Pred. No. 1.7e-07;  
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 AADPLHEAMRAAGDEFETRF 20  
 |||||:|||||:|||||  
 38 AADPLHQAMRAAGDEFETRF 57

Db

RESULT 6

BAB23468 PRELIMINARY; PRT; 193 AA.

ID BAB23468;

AC BAB23468;

DT 14-APR-2004 (TrEMBLrel. 27, Created)

DT 14-APR-2004 (TrEMBLrel. 27, Last sequence update)

DT 14-APR-2004 (TrEMBLrel. 27, Last annotation update)

DE Adult male lung cDNA, RIKEN full-length enriched library, clone:1200009L24 product:Bcl2-like 2, full insert sequence.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.



```
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RL 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
[4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RL prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
[5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RL sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Inotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shingawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RC EMBL; AK004680; BAB23468.1; -.
SQ SEQUENCE 193 AA; 20790 MW; 36CA185F5945DFB4 CRC64;
```

```
Query Match 97.1%; Score 101; DB 2; Length 193;
Best Local Similarity 95.0%; Pred. No. 1.7e-07;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 AADPLHEAMRAAGDEFETRF 20
Db 38 AADPLHEAMRAAGDEFETRF 57
```

```
RESULT 7
Q7TS60 PRELIMINARY; PRT; 219 AA.
AC Q7TS60;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE BCL-WEL.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=22672518; PubMed=12787069;
RA Itoh T., Itoh A., Pleasure D.;
RT "Bcl-2-related protein family gene expression during oligodendroglial
RL differentiation.";
RL J. Neurochem. 85:1500-1512(2003).
DR EMBL; AV185100; AAO64470.1; -.
DR GO; GO:0042981; P:regulation of apoptosis; IEA.
DR InterPro; IPR000712; Bcl2 BH.
DR InterPro; IPR003093; Bcl2 BH4.
DR InterPro; IPR002475; BCL2 family.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; BH4; 1.
DR PROSITE; PS00662; BCL2 FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01260; BH4; 1.
DR PROSITE; PS00663; BH4_2; 1.
SQ SEQUENCE 219 AA; 23720 MW; 30E36041BC1DC66F CRC64;
```

```
Query Match 97.1%; Score 101; DB 2; Length 219;
Best Local Similarity 95.0%; Pred. No. 1.9e-07;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 AADPLHEAMRAAGDEFETRF 20
Db 64 AADPLHEAMRAAGDEFETRF 83
```

```
RESULT 8
Q8CGL4 PRELIMINARY; PRT; 193 AA.
AC Q8CGL4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Bcl2-like protein 2.
GN Name=Bcl2l2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL; TISSUE=Skin;
RA Su H.-Y., Cheng W.T.K., Chen S.C., Lin C.T., Lien Y.Y., Liu H.J.,
RA Gilmour R.S.;
RT "Mouse keratinocytes express c99, a novel gene homologous to bcl-2,
RL that is stimulated by insulin-like growth factor 1 and prevents
RL dexamethasone-induced apoptosis.";
RL Biochim. Biophys. Acta 1676:127-137(2004).
DR EMBL; AV170344; AAO13177.2; -.
DR HSSP; Q52843; 100L.
DR MGD; MGI:108052; Bcl2l2.
DR GO; GO:0005515; P:protein binding; IPI.
DR GO; GO:0006915; P:apoptosis; IDA.
```

```

DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR003093; Bcl2_BH4.
DR InterPro; IPR002475; BCL2_family.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; BH4; 1.
DR PROSITE; PS00662; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01258; BH2; 1.
SQ SEQUENCE 193 AA; 20958 MW; 60D7F9E4DC56DFAE CRC64;

Query Match 88.5%; Score 92; DB 2; Length 193;
Best Local Similarity 85.0%; Pred. No. 4.1e-06;
Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AADPLHEAMRAAGDEFETRF 20
   |||||:|||||:|||||
Db 38 AADPLHQAMRAAGDELQTRF 57
   |||||:|||||:|||||

RESULT 9
Q6GP82 O6GP82 PRELIMINARY; PRT; 188 AA.
AC O6GP82;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932;
RA Srausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative";
RN Dev. Dyn. 225:384-391(2002).
[3]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Klein S., Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
EMBL; BC073259; AAF73259.1; -.

```

```

DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR003093; Bcl2_BH4.
DR InterPro; IPR002475; BCL2_family.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; BH4; 1.
DR PROSITE; PS00662; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
KW Hypothetical protein.
SQ SEQUENCE 188 AA; 20441 MW; CB3C1A8C55F16B96 CRC64;

Query Match 70.2%; Score 73; DB 2; Length 188;
Best Local Similarity 75.0%; Pred. No. 0.0037;
Matches 15; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 AADPLHEAMRAAGDEFETRF 20
   |||||:|||||:|||||
Db 33 ASICALHSAMRAAGDEFETRF 52
   |||||:|||||:|||||

RESULT 10
AR1_XENLA AR1_XENLA STANDARD; PRT; 228 AA.
AC Q91827;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 29-MAR-2004 (Rel. 43, Last annotation update)
DE Apoptosis regulator R1 (XRL) (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Head;
RX MEDLINE=95331613; PubMed=7607538;
RA Cruz-Reyes J., Tata J.R.;
RT "Cloning, characterization and expression of two Xenopus bcl-2-like
RT cell-survival genes";
RL Gene 158:171-179(1995).
CC !- FUNCTION: Could be the homolog of mammalian Bcl-W.
CC !- SUBCELLULAR LOCATION: Membrane-bound (potential).
CC !- DEVELOPMENTAL STAGE: Developmental regulation only occurs in the
CC brain of mid-metamorphic to post-metamorphic tadpoles and
CC adults, where an increase of several fold has been observed.
CC !- SIMILARITY: Belongs to the Bcl-2 family.
CC !- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC !- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC EMBL; X82462; CAA57845.1; -.
CC HSP; Q07817; IMAZ.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR003093; Bcl2_BH4.
DR InterPro; IPR002475; BCL2_family.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR PROSITE; PS00662; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
KW Apoptosis; Transmembrane.
FT NON TER 1
FT DOMAIN 120 139 BH1.

```

```

FT DOMAIN 171 186 BH2.
FT TRANSMEM 207 227 Potential.
SQ SEQUENCE 228 AA; 25068 MW; C499D449A585F8A9 CRC64;

Query Match 70.2%; Score 73; DB 1; Length 228;
Best Local Similarity 75.0%; Pred. No. 0.0044;
Matches 15; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AADPLHEAMRAAGDEFETRF 20
   : || || || || || || ||
   : || || || || || || ||
Db 73 ASCALHSAMRAAGDEFETRF 92

RESULT 11
Q8UWJ1 PRELIMINARY; PRT; 89 AA.
AC Q8UWJ1;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Bcl-x (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RA Shi Z., Onagbesan O.M., Williams J.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR GO; GO:0042981; P:regulation of apoptosis; IEA.
DR InterPro; IPR00712; Bcl2 BH.
DR InterPro; IPR002475; BCL2_family.
DR Pfam; PF00452; Bcl-2; 1.
DR SMART; SM00337; BCL; 1.
DR PROSITE; PS00662; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01259; BH3; 1.
DR NON_TER 1
FT NON_TER 89
FT SEQUENCE 89 AA; 10124 MW; B5B0EBE5F323A8C4 CRC64;

Query Match 51.9%; Score 54; DB 2; Length 89;
Best Local Similarity 52.6%; Pred. No. 1.6;
Matches 10; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 2 ADPLHEAMRAAGDEFETRF 20
   : : || || || || ||
   : : || || || || ||
Db 3 ASDVRQALRDAGDEFELRY 21

RESULT 12
BCLX CHICK
ID BCLX CHICK STANDARD; PRT; 229 AA.
AC Q07816; Q98908;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Apoptosis regulator Bcl-X (Bcl-2-like 1 protein).
GN Name=BCL2L1; Synonyms=BCLX, BCL-X;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM SHORT).
RX MEDLINE=93364977; Pubmed=8358789;
RA Boise L.H., Gonzalez-Garcia M., Postema C.E., Ding L., Lindsten T.,
RA Turka L.A., Mao X., Nunez G., Thompson C.B.;
RA "bcl-x, a bcl-2-related gene that functions as a dominant regulator of

```

```

RT apoptotic cell death.";
RL Cell 74:597-608(1993).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM LONG).
RC STRAIN=Hubbard White Mountain; TISSUE=Testis;
RX MEDLINE=97264485; Pubmed=9110311;
RA Vilagrasa X., Mezquita C., Mezquita J.;
RT "Differential expression of bcl-2 and bcl-x during chicken
   spermatogenesis.";
RL Mol. Reprod. Dev. 47:26-29(1997).
CC -I- FUNCTION: Dominant regulator of apoptotic cell death. The long
   form displays cell death repressor activity, whereas the short
   isoform promotes apoptosis (By similarity).
CC -I- SUBCELLULAR LOCATION: Mitochondrial membranes and perinuclear
   envelope (By similarity).
CC -I- ALTERNATIVE PRODUCTS.
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Long;
CC IsoId=Q07816-1; Sequence=Displayed;
CC Name=Short;
CC IsoId=Q07816-2; Sequence=VSP_000514;
CC -I- TISSUE SPECIFICITY: Highest expression in organs with lymphoid
   development.
CC -I- DOMAIN: BH4 domain seems to be involved in the anti-apoptotic
   function. Intact BH1 and BH2 domains are required for anti-
   apoptotic activity (By similarity).
CC -I- SIMILARITY: Belongs to the Bcl-2 family.
CC -I- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC -I- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC -I- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
CC -I- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
   between the Swiss Institute of Bioinformatics and the EMBL outstation -
   the European Bioinformatics Institute. There are no restrictions on its
   use by non-profit institutions as long as its content is in no way
   modified and this statement is not removed. Usage by and for commercial
   entities requires a license agreement (See http://www.isb-sib.ch/announce/
   or send an email to license@sib-sib.ch).
CC -----
CC EMBL; Z23110; CAA80657.1; -.
CC EMBL; U26645; AAB07677.1; -.
CC PIR; A47537; A47537.
CC HSSP; PS3563; 1AF3.
CC InterPro; IPR000712; Bcl2 BH.
CC InterPro; IPR003093; BCL2_BH4.
CC InterPro; IPR002475; BCL2_family.
CC InterPro; IPR004725; Bcl2_reg.
CC Pfam; PF00452; Bcl-2; 1.
CC Pfam; PF02180; BH4; 1.
CC TIGRFAMS; TIGR00865; bcl-2; 1.
CC PROSITE; PS50062; BCL2_FAMILY; 1.
CC PROSITE; PS01080; BH1; 1.
CC PROSITE; PS01258; BH2; 1.
CC PROSITE; PS01259; BH3; 1.
CC PROSITE; PS01260; BH4; 1.
CC PROSITE; PS50063; BH4_2; 1.
CC Alternative splicing; Apoptosis; Transmembrane.
KW DOMAIN 4 24 BH4.
FT DOMAIN 82 96 BH3.
FT DOMAIN 125 144 BH1.
FT DOMAIN 176 191 BH2.
FT TRANSMEM 206 223
FT VARSPPLIC 185 229
FT -----
SQ SEQUENCE 229 AA; 25733 MW; A97D3A4D04C0E9DA CRC64;

Query Match 51.9%; Score 54; DB 1; Length 229;
Best Local Similarity 52.8%; Pred. No. 4;
Matches 10; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 2 ADPLHEAMRAAGDEFETRF 20

```

Db 79 ASDVRAALRDAGDEFELRY 97  
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

## RESULT 13

Q9H1R5 PRELIMINARY; PRT; 125 AA.  
ID Q9H1R5  
AC Q9H1R5  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE BA243J16.1.2 (BCL2-like 1 (isoform 2)) (Fragment).  
GN Name=BCL2L1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Brown A.;  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL160175; CAC10004.1; -.  
DR HSSP; Q07817; 1LXL.  
DR GO; GO:0042981; P:regulation of apoptosis; IEA.  
DR InterPro; IPR000712; Bcl2 BH.  
DR InterPro; IPR003093; Bcl2\_BH4.  
DR InterPro; IPR002475; BCL2\_family.  
DR Pfam; PF00452; Bcl-2; 1.  
DR Pfam; PF02180; BH4; 1.  
DR SMART; SM00265; BH4; 1.  
DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
DR PROSITE; PS01259; BH3\_1.  
DR PROSITE; PS01260; BH4\_1; 1.  
DR PROSITE; PS50063; BH4\_2; 1.  
FT NON\_TER 125 125  
SQ SEQUENCE 125 AA; 13874 MW; D84C030651475365 CRC64;

Query Match 49.0%; Score 51; DB 2; Length 125;  
Best Local Similarity 64.3%; Pred. No. 6.5;  
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 7 EAMRAAGDEFETRF 20  
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |  
Db 88 QALREAGDEFELRY 101

## RESULT 14

Q9WUI5 PRELIMINARY; PRT; 170 AA.  
ID Q9WUI5  
AC Q9WUI5  
DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Bcl-x short.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Sprague-Dawley; TISSUE=Brain;  
RA He X.J., Jin K.L., Graham S.H., Simon R.P.;  
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF136230; AAD33683.1; -.  
DR HSSP; P53563; 1AF3.  
DR GO; GO:0042981; P:regulation of apoptosis; IEA.  
DR InterPro; IPR000712; Bcl2 BH.  
DR InterPro; IPR003093; Bcl2\_BH4.  
DR InterPro; IPR002475; BCL2\_family.  
DR Pfam; PF00452; Bcl-2; 1.  
DR Pfam; PF02180; BH4; 1.  
DR SMART; SM00337; BCL; 1.  
DR SMART; SM00265; BH4; 1.

DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
DR PROSITE; PS01259; BH3\_1.  
DR PROSITE; PS01260; BH4\_1; 1.  
DR PROSITE; PS50063; BH4\_2; 1.  
SQ SEQUENCE 170 AA; 19031 MW; B579ADAA98F79208 CRC64;

Query Match 49.0%; Score 51; DB 2; Length 170;  
Best Local Similarity 64.3%; Pred. No. 8.8;  
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 7 EAMRAAGDEFETRF 20

| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |  
Db 88 QALREAGDEFELRY 101

## RESULT 15

AAF81262 PRELIMINARY; PRT; 170 AA.  
ID AAF81262  
AC AAF81262  
DT 02-MAR-2004 (TrEMBLrel. 27, Created)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
DE Bcl-x short form.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Sprague-Dawley; TISSUE=cerebellum;  
RA Cao G., Chen J., Chen D.;  
RT "Bcl-Xs expression and its role in brain ischemia";  
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF279286; AAF81262.1; -.  
SQ SEQUENCE 170 AA; 18987 MW; D90868EC7F69ED59 CRC64;

Query Match 49.0%; Score 51; DB 2; Length 170;  
Best Local Similarity 64.3%; Pred. No. 8.8;  
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 7 EAMRAAGDEFETRF 20

| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |  
Db 88 QALREAGDEFELRY 101

Search completed: January 25, 2005, 10:10:35  
Job time : 134 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

## OM protein - protein search, using sw model

Run on: January 25, 2005, 10:06:02 ; Search time 24.5 Seconds  
(without alignments)  
78.544 Million cell updates/sec

Title: US-09-828-870-39

Perfect score: 104

Sequence: 1 AADPLHEAMRAAGDEFETRF 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:\*

1: PIR1.\*

2: PIR2.\*

3: PIR3.\*

4: PIR4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	51.9	190	2 A47537	apoptosis regulato
2	53.5	51.4	232	2 S24390	transforming prote
3	51	49.0	170	2 I49055	bcl-x short - mous
4	51	49.0	176	2 I67435	gene bcl-xshort pr
5	51	49.0	214	2 I49057	bcl-x transmembran
6	51	49.0	227	2 JE0203	apoptosis regulato
7	51	49.0	233	2 B47537	apoptosis regulato
8	51	49.0	233	2 I49056	bcl-x long - mouse
9	51	49.0	233	2 S51761	BCL-X protein - ra
10	51	49.0	233	2 I67431	BCL-X-Long - rat
11	50	48.1	216	2 B37332	transforming prote
12	50	48.1	233	2 A37332	transforming prote
13	49	47.1	610	2 A83638	probable glutamine
14	48	46.2	952	2 T36664	probable DNA topoi
15	48	46.2	1788	2 T29043	hypothetical prote
16	47	45.2	186	2 F86379	protein F2139.28 [
17	47	45.2	205	1 TVHU81	transforming prote
18	45	43.3	440	2 G70758	hypothetical prote
19	45	43.3	934	2 G70563	DNA topoisomerase
20	45	43.3	947	2 H86933	probable DNA topoi
21	45	43.3	1037	2 T13350	transcription fact
22	44	42.3	295	2 B83433	translocator prote
23	44	42.3	408	2 A82078	type IV pilin biog
24	44	42.3	507	2 JC7855	pyridoxine 4-oxida
25	44	42.3	596	1 WMBE2	UL32 protein - hum
26	44	42.3	866	2 C97365	he10 protein U4905
27	44	42.3	881	2 AE2153	DNA topoisomerase
28	44	42.3	898	2 S74903	DNA topoisomerase
29	44	42.3	1021	2 G75403	DNA topoisomerase

30 44 42.3 1601 2 AB1730 hypothetical prote  
31 43 41.3 127 2 T31206 hypothetical prote  
32 43 41.3 154 2 I58194 gene bcl-2 protein  
33 43 41.3 194 2 S51309 probable hypoxanth  
34 43 41.3 199 1 TVMSB1 transforming prote  
35 43 41.3 236 1 TVMSA1 transforming prote  
36 43 41.3 236 2 JC7383 B-cell lymphoma 2  
37 43 41.3 236 2 I67432 BCL-2 - rat (fragm  
38 43 41.3 236 2 I53744 gene bcl-2 protein  
39 43 41.3 239 1 TVHUA1 transforming prote  
40 43 41.3 337 2 G86594 hypothetical prote  
41 43 41.3 707 2 S50144 Gonyaulax-luciferi  
42 43 41.3 747 2 E84698 hypothetical prote  
43 43 41.3 1208 2 T42574 DNA-binding protei  
44 43 41.3 1231 2 S30185 insulin receptor s  
45 43 41.3 1235 1 S16948 insulin receptor s

## ALIGNMENTS

## RESULT 1

A47537

apoptosis regulator bcl-x - chicken

C;Species: Gallus gallus (chicken)

C;Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 09-Jul-2004

C;Accession: A47537

R;Boise, L.H.; Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.; Lindsten, T.; Turka, L.A.;

Cell 74, 597-608, 1993

A;Title: bcl-x, a bcl-2-related gene that functions as a dominant regulator of apoptot

A;Reference number: A47537; MUID:93364977; PMID:8358789

A;Accession: A47537

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-190 <BOI>

A;Cross-references: UNIPROT:Q07816; GB:223110; GB:I20120; NID:G510898; PIDN:CAA80657.1;

C;Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 51.9%; Score 54; DB 2; Length 190;

Best Local Similarity 52.6%; Pred.No. 0.53;

Matches 10; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 2 AADPLHEAMRAAGDEFETRF 20

Db 79 ASDVQRALRDAGDEFFELRY 97

## RESULT 2

S24390

transforming protein (Bcl-2) homolog - chicken

C;Species: Gallus gallus (chicken)

C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004

C;Accession: S24390

R;Cazals-Hatem, D.L.; Louie, D.C.; Tanaka, S.; Reed, J.C.

Biochim. Biophys. Acta 1132, 109-113, 1992

A;Title: Molecular cloning and DNA sequence analysis of cDNA encoding chicken homologue

A;Reference number: S24390; MUID:92379084; PMID:1511008

A;Accession: S24390

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-232 <CAZ>

A;Cross-references: UNIPROT:Q00709; EMBL:Z11961; NID:G62969; PIDN:CAA78018.1; PID:G6297

C;Superfamily: bcl apoptosis regulator, inhibitory type

C;Keywords: mitochondrion; transmembrane protein

Query Match 51.4%; Score 53.5; DB 2; Length 232;

Best Local Similarity 57.1%; Pred.No. 0.78;

Matches 12; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

Qy 1 AADPLHEAMRAAGDEFETRF 20

Db 81 AADPGVHLALRQAGDEFESRY 101

```

RESULT 3
I49055
bcl-x short - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I49055
R;Fang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.
J. Immunol. 153, 4388-4398, 1994
A;Title: Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes.
A;Reference number: I49055; MUID:95052604; PMID:7963517
A;Accession: I49055
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-170 <RES>
A;Cross-references: UNIPROT:Q64373; EMBL:U10102; NID:g506645; PIDN:AAA82172.1; PID:g5066
C;Genetics:
A;Gene: bcl-x
C;Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 49.0%; Score 51; DB 2; Length 170;
Best Local Similarity 64.3%; Pred. No. 1.4;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 7 EAMRAAGDEFETRF 20
      :|:| | | | | | | |
Db 88 QALREAGDEFELRY 101

RESULT 4
I67435
gene bcl-xshort protein - rat (fragment)
C;Species: Rattus sp. (rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 28-Jul-2003
C;Accession: I67435
R;Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L.
Endocrinology 136, 232-241, 1995
A;Title: Expression of members of the bcl-2 gene family in the immature rat ovary: equin
onstitutive bcl-2 and bcl-xlong messenger ribonucleic acid levels.
A;Reference number: I53295; MUID:95129487; PMID:7828536
A;Accession: I67435
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-176 <RES>
A;Cross-references: GB:S78284; NID:g998483; PIDN:AAC60702.1; PID:g998484
C;Genetics:
A;Gene: bcl-x
C;Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 49.0%; Score 51; DB 2; Length 176;
Best Local Similarity 64.3%; Pred. No. 1.4;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 7 EAMRAAGDEFETRF 20
      :|:| | | | | | |
Db 94 QALREAGDEFELRY 107

RESULT 5
I49057
bcl-x transmembrane deleted - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I49057
R;Fang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.
J. Immunol. 153, 4388-4398, 1994
A;Title: Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes.
A;Reference number: I49055; MUID:95052604; PMID:7963517
A;Accession: I49057
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-214 <RES>
A;Cross-references: UNIPROT:Q64373; EMBL:U10102; NID:g506649; PIDN:AAA82174.1; PID:g5066

```

```

C;Genetics:
A;Gene: bcl-x-long
C;Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 49.0%; Score 51; DB 2; Length 214;
Best Local Similarity 64.3%; Pred. No. 1.8;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 7 EAMRAAGDEFETRF 20
      :|:| | | | | | |
Db 88 QALREAGDEFELRY 101

RESULT 6
JE0203
apoptosis regulator bcl-x isoform - human
N;Alternate names: h-bcl-xbeta
C;Species: Homo sapiens (man)
C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 09-Jul-2004
C;Accession: JE0203
R;Ban, J.; Eckhart, L.; Weninger, W.; Mildner, M.; Tschachler, E.
Biochem. Biophys. Res. Commun. 248, 147-152, 1998
A;Title: Identification of a human cDNA encoding a novel bcl-x isoform.
A;Reference number: JE0203; MUID:98340865; PMID:9675101
A;Accession: JE0203
A;Molecule type: mRNA
A;Residues: 1-227 <BAN>
A;Cross-references: UNIPROT:Q07817; GB:U72398; NID:g1622940; PIDN:AAB17354.1; PID:g1622.
C;Genetics:
A;Gene: bcl-x
A;Map position: 20
C;Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 49.0%; Score 51; DB 2; Length 227;
Best Local Similarity 64.3%; Pred. No. 1.9;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 7 EAMRAAGDEFETRF 20
      :|:| | | | | | |
Db 88 QALREAGDEFELRY 101

RESULT 7
B47537
apoptosis regulator bcl-xL - human
N;Alternate names: bcl-2-related protein
N;Contains: apoptosis regulator bcl-xs
C;Species: Homo sapiens (man)
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C;Accession: B47537; C47537
R;Boise, L.H.; Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.; Lindsten, T.; Turka, L.A.;
Cell 74, 597-608, 1993
A;Title: bcl-x, a bcl-2-related gene that functions as a dominant regulator of apoptot:
A;Reference number: A47537; MUID:93364977; PMID:8358789
A;Accession: B47537
A;Status: nucleic acid sequence not shown; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-233 <BOI>
A;Cross-references: UNIPROT:Q07817; GB:IL20121; NID:g510900; PIDN:CAA80661.1; PID:g510900
A;Accession: C47537
A;Status: nucleic acid sequence not shown; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-69, 'G', 71-125, 189-233 <BO2>
A;Cross-references: GB:IL20122; NID:g623236; PIDN:CAA80662.1; PID:g623237
C;Genetics:
A;Gene: GDB:BCL2L
A;Cross-references: GDB:228079
C;Superfamily: bcl apoptosis regulator, inhibitory type
C;Keywords: alternative splicing; apoptosis
F;1-233/Product: apoptosis regulator bcl-xL #status predicted <MAT>
F;1-125,189-233/Product: apoptosis regulator bcl-xs #status predicted <MA2>

Query Match 49.0%; Score 51; DB 2; Length 233;

```

Best Local Similarity 64.3%; Pred. No. 1.9; Mismatches 3; Indels 2; Gaps 0;  
Matches 9; Conservative 3; Indels 0; Gaps 0;

QY 7 EAMRAAGDEFETRF 20  
Db 88 QALREAGDEFELRY 101

RESULT 8  
I49056  
bcl-x long - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C;Accession: I49056; S52866  
R;Fang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.  
J. Immunol. 153, 4388-4398, 1994  
A;Title: Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes.  
A;Reference number: I49055; MUID:9502604; PMID:7963517  
A;Accession: I49056  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-233 <RES>  
A;Cross-references: UNIPROT:Q64373; EMBL:U10101; NID:9506647; PIDN:AAA82173.1; PID:g5066  
R;Kamesaki, H.; Michaud, G.F.; Takatsu, K.; Okuma, M.  
submitted to the EMBL Data Library, November 1994  
A;Description: IL-5 inhibits anti-IgM-induced apoptosis in an immature B cell line throu  
A;Reference number: S52866  
A;Accession: S52866  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-233 <KAM>  
A;Cross-references: EMBL:X83574; NID:g695622; PIDN:CAA58557.1; PID:g695623  
C;Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 49.0%; Score 51; DB 2; Length 233;  
Best Local Similarity 64.3%; Pred. No. 1.9;  
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 7 EAMRAAGDEFETRF 20  
Db 88 QALREAGDEFELRY 101

RESULT 9  
S51761  
BCL-X protein - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 07-May-1995 #sequence\_revision 01-Sep-1995 #text\_change 09-Jul-2004  
C;Accession: S51761; S51762  
R;Michaelidis, T.M.  
submitted to the EMBL Data Library, November 1994  
A;Reference number: S51761  
A;Accession: S51761  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-233 <MIC>  
A;Cross-references: UNIPROT:P53563; EMBL:X82537; NID:g607176; PIDN:CAA57886.1; PID:g6071  
A;Experimental source: embryonic; brain  
A;Accession: S51762  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-125,189-233 <MI2>  
A;Cross-references: EMBL:X82537; NID:g607176; PIDN:CAA57887.1; PID:g607178  
A;Experimental source: embryonic; brain  
A;Note: smaller form due to splicing  
C;Genetics:  
A;Introns: 125/3  
C;Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 49.0%; Score 51; DB 2; Length 233;  
Best Local Similarity 64.3%; Pred. No. 1.9;  
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 7 EAMRAAGDEFETRF 20  
Db 88 QALREAGDEFELRY 101

RESULT 10  
I67431  
BCL-X long - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 09-Jul-2004  
C;Accession: I67431  
R;Filly, J.L.; Filly, K.I.; Kenton, M.L.; Johnson, A.L.  
Endocrinology 136, 232-241, 1995  
A;Title: Expression of members of the bcl-2 gene family in the immature rat ovary: equi  
onstitutive bcl-2 and bcl-x long messenger ribonucleic acid levels.  
A;Reference number: I53295; MUID:95129487; PMID:7828536  
A;Accession: I67431  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-233 <RES>  
A;Cross-references: UNIPROT:P53563; EMBL:U34963; NID:g1004376; PIDN:AAA77686.1; PID:g10  
C;Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 49.0%; Score 51; DB 2; Length 233;  
Best Local Similarity 64.3%; Pred. No. 1.9;  
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 7 EAMRAAGDEFETRF 20  
Db 88 QALREAGDEFELRY 101

RESULT 11  
B37332  
transforming protein (bcl-2-beta) - chicken  
C;Species: Gallus gallus (chicken)  
C;Date: 03-Mar-1993 #sequence\_revision 03-Mar-1993 #text\_change 28-Jul-2003  
C;Accession: B37332; S35452  
R;Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.  
Nucleic Acids Res. 20, 4187-4192, 1992  
A;Title: Isolation and characterization of the chicken bcl-2 gene: expression in a vari  
A;Reference number: A37332; MUID:92375724; PMID:1508712  
A;Accession: B37332  
A;Status: nucleic acid sequence not shown  
A;Molecule type: DNA  
A;Residues: 1-216 <EGU>  
A;Cross-references: EMBL:D11381; EMBL:D11382  
C;Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 48.1%; Score 50; DB 2; Length 216;  
Best Local Similarity 56.2%; Pred. No. 2.5;  
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 5 LHEAMRAAGDEFETRF 20  
Db 87 VHLALRQAGDEFERRY 102

RESULT 12  
A37332  
transforming protein (bcl-2-alpha) - chicken  
C;Species: Gallus gallus (chicken)  
C;Date: 03-Mar-1993 #sequence\_revision 03-Mar-1993 #text\_change 09-Jul-2004  
C;Accession: A37332; S35453  
R;Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.  
Nucleic Acids Res. 20, 4187-4192, 1992  
A;Title: Isolation and characterization of the chicken bcl-2 gene: expression in a vari  
A;Reference number: A37332; MUID:92375724; PMID:1508712  
A;Accession: A37332  
A;Status: nucleic acid sequence not shown  
A;Molecule type: DNA  
A;Residues: 1-233 <EGU>  
A;Cross-references: UNIPROT:Q00709; EMBL:D11381

## C;Genetics:

A;Introns: 189/3  
 A;Superfamily: bcl apoptosis regulator, inhibitory type  
 C;Keywords: mitochondrion; transforming protein; transmembrane protein

Query Match 48.1%; Score 50; DB 2; Length 233;  
 Best Local Similarity 56.2%; Pred. No. 2.7;  
 Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 5 LH5AMRAAGDEFETRF 20  
 :||:|||||:  
 Db 87 VHLALRQAGDEFGRY 102

## RESULT 13

A83638  
 probable glutamine amidotransferase PA0051 [imported] - Pseudomonas aeruginosa (strain H  
 C;Species: Pseudomonas aeruginosa  
 C;Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004

C;Accession: A83638  
 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B  
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lam,  
 ; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000  
 A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho  
 A;Reference number: A82950; MUID:20437337; PMID:10984043

A;Accession: A83638  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-610 <STO>  
 A;Cross-references: UNIPROT:Q9T781; GB:AE004445; GB:AE004091; NID:g9945872; PIDN:AAG0344  
 A;Experimental source: strain PA01

C;Genetics:  
 A;Gene: PA0051

Query Match 47.1%; Score 49; DB 2; Length 610;  
 Best Local Similarity 58.8%; Pred. No. 11;  
 Matches 10; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 3 DPLHEAMRAAGDEFETR 19  
 |||||:  
 Db 85 DALRLRLRAGHEFTR 101

## RESULT 14

T36664  
 probable DNA topoisomerase I - Streptomyces coelicolor  
 C;Species: Streptomyces coelicolor  
 C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004

C;Accession: T36664  
 R;Seeger, K.J.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
 submitted to the EMBL Data Library, March 1999

A;Reference number: Z21611  
 A;Accession: T36664

A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA

A;Residues: 1-952 <SEE>  
 A;Cross-references: UNIPROT:Q9X909; EMBL:AL035636; PIDN:CAB38480.1; GSPDB:GN00070; SCOE  
 A;Experimental source: strain A3(2)

C;Genetics:  
 A;Gene: SCOEDB:SCH5.06c  
 C;Superfamily: bacterial type I DNA topoisomerase

Query Match 46.2%; Score 48; DB 2; Length 952;  
 Best Local Similarity 52.9%; Pred. No. 24;  
 Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 ADPLHEAMRAAGDEFET 18  
 |||||:  
 Db 377 AQEAHEAIRPSGDRFT 393

## RESULT 15

## T29043

hypothetical protein B0228.2 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans  
 C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
 C;Accession: T29043

R;Leimbach, D.  
 submitted to the EMBL Data Library, March 1995  
 A;Description: The sequence of C. elegans cosmid B0228.

A;Reference number: Z18324  
 A;Accession: T29043  
 A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-1788 <LEI>  
 A;Cross-references: UNIPROT:Q8IG61; EMBL:U23168; PIDN:AAC38806.1; CESP:B0228.2

A;Experimental source: strain Bristol N2  
 C;Genetics:

A;Introns: 1456/2; 1482/3; 1516/2; 1551/3; 1595/3; 1646/1; 1671/1; 1716/2; 1749/3

Query Match 46.2%; Score 48; DB 2; Length 1788;  
 Best Local Similarity 50.0%; Pred. No. 47;  
 Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 2 ADPLHEAMRAAGDEFETR 19  
 |||||:  
 Db 628 AKTLHEARKSGQTFETK 645

Search completed: January 25, 2005, 10:27:40  
 Job time : 25.5 secs